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RESULT 1
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Sequence 19 from patent AR146579 AR146579.1 GI:15109768

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PAT 08-AUG-2001

AR146579

REFERENCE AUTHORS

Obata, Y.

(bases 1 to 714)

Unknown. Unclassified Unknown.

TITLE JOURNAL

Isolated nucleic acid molecules associated with gastrić cancer and methods for diagnosing and treating gastric cancer Patent: US 6218521-A 19 17-APR-2001;

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SUMMARIES

Result No. a იი G 0000 00 იიი Score Match 15129 5 160701 5 1712404 5 185185 5 188885 5 188885 5 192925 5 11297 5 211297 5 211297 5 21220 5 23824 9 133016 9 133016 9 133016 1500 1 2661 4 2599 3 145564 2571 2 2676 1 248677 Length B 210 BR146579 BAR146579 BAR146583 AL345183 ACC022723 AL445183 ACC025931 AR146582 ABC0079829 BD079829 HWMSTEAA AR146582 BD079829 HWMSTEAA AR146582 AF051897 AC134729 AR7367XDA BC0183844 BC018384420 BR06138842 AC138842 AC138842 AC138842 AC138842 AC138842 AC138842 AC138842 AC138842 AC138832 AC138832 AC138832 AC138833 ALIGNMENTS M75884 Human stero AF051897 Oryctolag M62763 Rat 60 kDa AC134794 Mus muscu M57453 Rat sterol BC018384 Mus muscu AR24406 Mus muscu AR246194 Sequence 89 AR7382 Sequence 89 AR7382 Sequence 89 AC13848 Homo sapi AC138848 Homo sapi AC138848 Homo sapi AC138850 Homo sapi AC138851 Homo sapi AC138852 Homo sapi AC138852 Homo sapi AC138853 Homo sapi AC138854 Homo sapi AC138854 Homo sapi AC138855 Homo sapi AC138855 Homo sapi AC138856 Homo sapi AC138851 Homo sapi AC138551 Homo sapi AC138851 Homo sapi AC138851 Homo sapi AC138851 Homo sapi AC138851 Homo sapi AC022728 Homo sapi AL445183 Human DNA BC005911 Homo sapi AR146580 Sequence BD079829 Cancer-as S52420 sterol carr M55421 Human stero AR146582 Sequence BD079831 Cancer-as AC025535 AE014828 AX599046 Sequence AC115599 Dictyoste U17009 Phytophthor U11313 Human stero M75883 Human stero AL358233 Homo sapi BD079828 Cancer-as AR146579 Sequence Description Homo sapi sapi

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Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 714) old,L.J., Scanlan,M.J., Stockert,E., Gure,A., Chen,Y.T., Cochare,M., Obata,Y., Pfreundschuh,M., Tureci,O. and Sahin,
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Cancer-associated nucleic acids and polypeptides Patent: JP 2001515009-A 494 25-SEP-2001; LUDWIG INSTITUTE FOR CANCER RESEARCH OS Homo sapiens (human)
PN UP 2001516009-A/494
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PR 17-JUL-1997 US 08/896164,10-CCT-1997 US
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11-OCT-1997 GB 9721697.2,22-JUN-1998 US 09/102322 PI
OLD, MATTHEW J SCANLAN, ELISABETH STOCKERT, ALI GURE, YAO PI
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llarity 100.0%;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
100 c 92 g 26
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(SCP-X/SCP-2) (
U11313
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Submitted (24-UN-1994) Jerome P. Strauss III, Department of Submitted (24-UN-1994) Jerome P. Strauss III, Department of Obstetrics and Gynecology, Division of Reproductive Biology, University of Pennsylvania Medical Center, 778 Clinical Research Building, 422 Curie Boulevard, Philadelphia, PA 19104-6142, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohba, T., Rennert, H., Pfeifer, S.M., He, Z., Yamamoto, R., Holt, J.A., Billheimer, J.T. and Strauss, J.F. III.

The structure of the human sterol carrier protein X/sterol carrier protein 2 gene (SCP2)

Genomics 24 (2), 370-374 (1994)
95213031
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Strauss, J.F. III.
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1. (bases 1 to 1052)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/chromosome="1"
/map="1932"
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U11301.1:26...157,U11302.1:26...90,U11303.1:26...152,
U11304.1:26...89,U11305.1:26...112,U11306.1:26...176,
U11307.1:26...173,U11308.1:26...133,U11309.1:1547...1700
U11310.1:26...128,U11311.1:26...155,U11312.1:26...105,
26...121)
                                                                                                                                                                                                                                 /partial
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U11304.1:26...89,U11305.1:26...112,U11306.1:26...176,
U11307.1:26...173,U11308.1:26...133,U11309.1:1547...1700,
U11310.1:26...128,U11311.1:26...155,U11312.1:26...105,
26...1034)
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U11307.1:1..198,U11308.1:1..158,U11309.1:1..1725,

U11310,1:1..153,U11311.1:1..180,U11312.1:1..130,1.
                                                                                                                                                                        /gene="SCP-X/SCP-2"
/product="sterol cap
protein-2"
/gene="SCP-X/SCP-2"
/codon_start=1
/product="sterol_carrier
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protein-X/sterol
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                                                                 CCAGACCATAATTACCATATTAACTTTGTTNTGCACAGTTGTTTGCCAATTC
                                                                                                                                        GTTTACATAGTTCTTTGGGATTTTTACTGTTCCTAATTTTATTCTGAAACTCAATTTTACC
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LTILQCCPTSDGAAAAILASBAFVQKYGLQSKAVEILAQEMMTDLPSSFEEKSIIKMV
GFDMSKEAARKCYEKSGLTPNDIDVIELHDCFSTNELLTYEALGLCPEGQGATLVDRG
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FVKKIGGIFAFKVKDGFGGKBATWVVDVKNGKGSVLPNSDKKADCTITMADSDFLALM
TGKMNPQSAFFQGKLKITGNMGLAMKLQNLQLQPGNAKL"
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/note="nucleotides :
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Pred. No. 3e-88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Dec 6, 1993 this sequence version replaced gi:410029. Original source text: Human liver cDNA to mRNA. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 2572)
Vesa, J., Hellsten, E., Branoski, B.L., Emanuel, B.S., Billheimer, Mead, S., Cowell, J.K., Strauss, J.F.III. and Peltonen, L.
Assignment of sterol carrier protein X/sterol carrier protein
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1 (bases 1 to 2572)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/gene="SCP-X/SCP-2"
/evidence=experimental
2572
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//db_xref="G1:432975"
//db_xref="G1:43297
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/~lone_lib="Clontech
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/evidence=not_experimental
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/mol_type="mRNA"
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/evidence=experimental
439 c 570 g
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                                                                                      Chordata;
Primates;
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Pred. No. 2.2e-88;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ω
                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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SEQUENCING IN
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481

2152 421 2212 361

2272

301

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241 2392 181 2452 121

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FEATURES
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                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 20% of reads Chemistry
Dye-terminator Big Dye; 79% of reads
Consensus quality: 118880 bases at least Q40
Consensus quality: 120216 bases at least Q30
Consensus quality: 120979 bases at least Q20
Insert size: 136681; 7.7% error; agarose-fp
Quality coverage: 4.05x in Q20 bases; sum-of-contigs Quality
Coverage: 3.75x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone request@sanger.ac.uk
On Aug 12, 2000 this sequence version replaced gi:9214208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: dJ835A17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Sanger Centre
Center code: SC
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13587
30894
30994
37023
37123
37123
45382
45482
56889
56889
84392
117844
117944
                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="taxon:9606"
/chromosome="1"
/clone="RP5-835A17"
                                                                                                                                                                                                                                                               /note="assembly_fragment:01065
fragment_chain:1"
13587. .30893
                                                                                                              fragment
                                                                                                                                                                     /note="assembly_fragment:00153
fragment_chain:1"
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 /note="assembly_fragment:00192'
34492. .117843
                                                       /note="assembly_fragment:00948
fragment_chain:2"
                                                                                                                                 note="assembly_
                                                                                                                                                                                                                            /note="assembly_fragment:00181
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location,
                                                                                                                                                                                                                                                                                                                                            clone_lib="RPCI-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13486: contig of 13486 bp in length
13586: gap of 100 bp
30893: contig of 17307 bp in length
30993: gap of 100 bp
37022: contig of 6029 bp in length
37122: gap of 100 bp
45381: contig of 8259 bp in length
45481: gap of 100 bp
56788: contig of 11307 bp in length
46888: gap of 100 bp
84391: contig of 27503 bp in length
84491: gap of 100 bp
117843: contig of 3352 bp in length
117943: gap of 100 bp
117943: gap of 100 bp
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REFERENCE
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AC022728/c
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 175046)
                                                                                                                                                           175046 bp
Homo sapiens chromosome 1 clone
SEQUENCE, 34 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT Homo sapiens (human)
                                                                                                                             AC022728
AC022728.4 GI:7249198
                                                                        Homo sapiens
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31142 a 30481 c 29651 g 30201 t
                                                                                                                                                                                                                                                                                                      CCAGACCATAATTACCATATTAACTTTGTAATGCACAGTTGTATGCAATTCC 47990
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117944. .122176
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Pred. No. 5.6e-89;
0; Mismatches 11
Nusbaum, C. and Lander, E
                                                                                                                                                                                      DNA linear
RP11-310J14 map 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will

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REFERENCE
AUTHORS
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Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,

Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,

Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

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Gandopiano, A., Castle, A., Coyette, M., Gage, D.,

Galagan, J., Gardyna, S., Ginde, S., Gyvette, M., Graham, L.,

Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,

Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehoczky, J.,

McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,

McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,

Murphy, T., Naylor, J., Norman, C. H., O'Connot, T., O'Donnell, P.,

O'Neil, D., Olivar, T., M., Oliver, J., Peterson, K., Pierre, N.,

Pisani, C., Pollara, V., Raymond, C., Rieley, R., Rogov, P., Rothman, D.,

Pov A. Santos R. Schaner, S. Severy D. Spencer, R.
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* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 16, 2000 this sequence version replaced gi:6980310. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Direct Submission
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                                                                                                        Quality coverage: 3.4 in Q20 bases; agarose-fp Quality coverage: 3.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                     Center project name: L5491
Center clone name: 310 J 14
Center clone name: 310 J 14
Sequencing vector: M13, M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 156135 bases at least Q40
Consensus quality: 165373 bases at least Q30
Consensus quality: 16980 bases at least Q20
                                                                                                                                                                                                       Insert size: 185000; agarose-fp Insert size: 171746; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
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9102. .10622
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6174. ..7552
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16361. .18265
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Location/Qualifiers
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15050. .16260
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13499. .14949
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7653. .9001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 672.8;
Pred. No. 4.9
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AUTHORS
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                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                           where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at the property of the sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42818
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Human DNA
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AL445183
                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1 constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
RP11-334A14 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 7. 2002 this sequence version replaced gi:17939714.
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wallis,J.
Direct Submission
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                          VECTOR: pBACe3.6.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                       Location/Qualifiers
1. .193774
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Primates;
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RESULT 8
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Best Local Similarity
Matches 699; Conserv
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1 (bases 1 t
Strausberg, R.
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1439)
                                                                                                              Homo sapiens, sterol IMAGE:4287946, mRNA,
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                                                  Homo sapiens
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                                                             sapiens (human)
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/clone="RP11-334A14"
/clone_lib="RPCI-11.2"
/45351 c 44031 g 53577
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Pred. No. 4.7e-89;
0; Mismatches 11
                                                                                                                                    mRNA
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Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 21 Row: n Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 432978.

Location/Qualifiers
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http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission

Direct Submission

Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Contact: MGC help desk
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                                       AATATTTTTATTTTAAAAAATAAGCCTGTGTTCAAGCTCTGATCATATTTCTTTTATTTTTG 363
                                                                                                                                                 CTTAATGATGGTGTTTTATGACTAATACACTGATTTTTCAAGAAGGAAACCCATGTTAAA
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   AATATTTTATTTTAAAAAATAAGCCTGTGTTCAAGCTCTGATCATATTTCTTTTATTTTG
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/mol type="mRNA"
/db xref="LocusID:6342"
/db xref="LocusID:636"
/clone="MGC:14505 IMAGE:4287946"
/tissue_type="Brain, primitive neu:/clone_lib="NNH_MGC_56"
/lab_host="HH10B"
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ZOPVKKIGGIFAFKVKUGPGGKEATWVDVKNGKGSVLENSDKKADCTITMADSDFLA
LMTGKNNEPGSAFFQGKKLTGNMGLAMKLQNLQLQPGNAKL"
219 c 272 g 458 t
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/protein_id="AAH05911.1"
/db_xref="GI:13543503"
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Pred. No. 1.5e-87;
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Sequence 20
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                  TTTAAAAATAAGCCTGTGTTTCAAGCTCTGATCATATTTCTTTTATTTTTGATTTTGGGAANA
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JP 2001516009-A/495.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                         PI UGUR SAHIN

PC G01N33/574, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00, A61P35/00, C07K16/82, C07K16/32, C12N15/09//C07K16/46, C12P21/08, A61K37/0PC C12N15/00

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PR 17-JUL-1997 US 08/896164,10-OCT-1997 US 60/061599
PR 17-JUL-1997 US 60/061765,10-OCT-1997 US 08/948705 PR 10-OCT-1997 US 09/102322 PI 1-OCT-1997 GB 9721697.2,22-JUN-1998 US 09/102322 PI JOLD,MATTHEW J SCANLAN,ELISABETH STOCKERT,ALI GURE,YAO PI
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 687)
Old,L.J., Scanlan,M.J., Stockert,E., Gure,A., Chen,Y.T., Gout,I., Schol,L.J., Scanlan,M.J., Stockert,E., Tureci,O. and Sahin,U. Oghare,M., Obata,Y., Pfreundschuh,M., Tureci,O. and Sahin,U. Cancer-associated nucleic acids and polypeptides
Patent: JP 2001516009-A 495 25-SEP-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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JP 2001516009-A/495
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                                                                                                                                                             Location/Qualifiers
                                                                                                                /organism='Homo
                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 122504] from the original journal article. This sequence comes from Fig. 1.
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Mammalia; Eutheria; Primates;
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M55421.1 GI:432978
sterol carrier protein-2.
Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

Human sterol M55421

carrier

1219 bp protein-2 (

(SCP-2) m

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PRI 06-DEC-1993

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/protein_id="AAB24921.1"
/brotein_id="AAB24921.1"
/db_xref="G1:263551"
/tamslation="MGFPAASSFRTHQIEAVPTSSASDGFKANLVFKEIEKKLEEEG
/translation="RFKVKDFPEGKEDTWVDVKNGQGSVLPNSKKADCTITMAASDFLA
LMTGKMNDQSAFFQGPLKITGNMGLAMKLQNLQLQPGNAKL"
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Yamamoto,R., Kallen,C.B., Babalola,G.O., Rennert,H.,
Billheimer,J.T. and Strauss,J.F. III.
Cloning and expression of a cDNA encoding human sterol
protein 2
Proc. Natl. Acad. Sci. U.S.A. 88 (2), 463-467 (1991)
                                                                                                                                                                                          Similarity
               TAAGCCTGTGTTCAAGCTCTGATCATATTTCTTTTATTTTGATTTTGGAANAAAATACTG
                                                            GACTAATACACTGATTTTCAATAAGGAAACCCATGTTAAAAATATTTTTATTTTAAAAA
                                                                          GACTAATACACTGATTTTTCAAGAAGGAAACCCATGTTAAAAATATTTTTTATTTTAAAAA
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1062. .1067
/gene="SCP-2"
/evidence=not_experimental
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/evidence=experimental
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EQFVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPNSDKKADCTITMADSDFLA
IMTGKNNPQSAFFQGKLKITGNNGLAMKLQNLQLQPGNAKL"
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84. .515
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/evidence=experimental
195 c 255 g
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/codon_start=1
/product="sterol carrier protein-2"
/protein_id="AAA03559.1"
/db_xref="GI:432973"
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144. .512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="1p32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SCP-2"
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0; Mismatches 11;
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                                           TGCAGATAATTAAACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATA
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PR 17-JUL-1997 US 08/896164,10-OCT-1997 US 60/061599
10-OCT-1997 US 60/061765,10-OCT-1997 US 08/948705 PR
11-OCT-1997 GB 9721697.2,22-JUN-1998 US 09/102322 PI
JOLD, MATTHEW J SCANLAN, ELISABETH STOCKERT, ALI GURE, YAO PI
                                                                                                                                                                                                         PI UGUR SAHIN

PC

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GC1N33/574, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00, A61P35/00, A61P35/
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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JOURNAL MEDLINE PUBMED DNA Cell 92029618 1718316 He,Z., Yamamoto,R., Furth,E.E., Schantz,L.J., Naylor,S.L., George,H., Bilheimer,J.T. and Strauss,J.F. III.

cDNAs encoding members of a family of proteins related to human sterol carrier protein 2 and assignment of the gene to human chromosome 1 p21----pter Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1500) sterol carrier protein-2.
Homo sapiens (human)
Homo sapiens M75884.1 GI:432976 Human sterol Biol. carrier protein 10 (8), 59 559-569 (1991) 1500 2 ရွ mRNA, complete cds. mRNA linear

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JOURNAL COMMENT
Search completed: November 27, Job time: 2896.94 secs
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Assignment of sterol carrier protein X/sterol carrier protein 2 to 1932 and exclusion as the causative gene for infantile neuronal cesoid lipofusionosis
Unpublished
On Dec 6, 1993 this sequence version replaced gi:337996.
Original source text: Human liver cDNA to mRNA.
                                                                                                    ACCCCAGACCATAATTACCATATTAACTTTGTTNTGCACAGTTGTTTTGCCAATTC 713
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/gene-"SCP-2"
/note-"no polyA or polyA signal was found this cDNA clone, indicating that the mRNA partial at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MMTDLPSSFEEKSIIKMVGFDMSKEAARKCYEKSGLTPNDIDVIELHDCFSTNELLTYEALGLCPEGGATLVDTGDDNYGGKWJUNDSGGLISKGHPLGATGLAGCAELKWGLGFEAKSVERTHGLAGCAELKWGLGFEAKSVERTHGLAGCAELKWGFEEKAKOVEGKKVALQHNLGIGGAVVVTLYKWGFEEKALSKERTHVVIENTYSSASDGFKANLVFKEIEKKLEEEGEQFVKKIGGIFAFKVKDGPGGKEATWVV
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LQNLQLQPGNAKL"
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/codon_start=1
/product="sterol carrier protein-2"
/protein_id="AAA03558.1"
/db_xref="GI:432977"
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/mol_type="mRNA"
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/map="1p32"
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/clone_Tib="Clontech HL-1001b;HL-1115b"
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AI826287 wk33f07.x
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65988 tn5	156	9	9		634.4	23
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ALIGNMENTS

REFERENCE AUTHORS TITLE SOURCE ORGANISM ACCESSION VERSION RESULT 1 BQ014192 LOCUS COMMENT KEYWORDS DEFINITION JOURNAL Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library harayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 317-343, >AT_rich#Low_complexity (matched compliment) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 769) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Homo sapiens BQ014192 BQ014192.1 GI:19739093 EST. BQ014192 769 bp mRNA linear EST 26-MAR. UI-H-ED1-axs-g-24-0-UI.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone IMAGE:5833007 3', mRNA sequence. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens (human) EST 26-MAR-2002

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542 ATTGAATCTTCAGCAGAATAATCCTTAAATATACTTTGTAAGCAAAACAAAAGCTTTTTT
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                                         TTACTGGCCAGCTGTTGGCATTGTGTTTCTTACTTAGTTCTCCCAA-GGAAAACTCTTAA
                                                                 TTACTGGCCAGCTGTTGGCATTGTGTTTCTTACTTTAGTTCTCCCAAGGGAAAACTCTTAA
                                                                                                                           TCTCACTAATTTTAAGAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="Chondrosarcoma"
//dev_stage="Adult"
//dev_stage="Adult"
//lab_host="DH108 (Life Technologies)"
//clone_lib="WCI_CCAP_ED1"
//clone_lib="WCI_CCAP_ED1"
//note="Torgan: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line_CS5. The library was constructed according to Bonaldo
, Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dr
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
sequence tag for this library is GCTCAAGGCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAG_TISSUE=chondrosarcoma
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db_xref="taxon:9606"
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iow

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

The following repetitive elements were found in this cDNA

sequence: 316-342, >AT rich#Low_complexity (matched compliment)

morve are complexed.
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UI-H-ED0-axo-f-03-0-UI.sl NCI_CGAP_ED0 Homo sapiens cDNA clone
IMAGE:5831426 3', mRNA sequence.
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                                                                                                                                                                                                                           /clone lib=NCI CGAP EDO"
//clone lib=NCI CGAP EDO"
//clone = "Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a moddfied polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP EDO is a cDNA library containing
the Following tissue(s): Chondrosarcoma cell line CS5. The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
                                                                                                        TAG_LIB=UI-H-ED0
TAG_TISSUE=chondrosarcoma
TAG_SEQ=CGTCAAGGCT"
108 c 98 g 285
                                                                                                                                                                                                             library is GCTCAAGGCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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  94.2%;
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  Score 672.8; DB 12; Length 761; Pred. No. 7.4e-70;
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                                                                                                       Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrat Eukaryota; Metazoa; Chordata; Catarrhini; Hominid 1 (Dases 1 to 821)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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#821 bp mRNA linear EST 16-DEC-1999
##829f11.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2299533 3'
similar to gb:\(\overline{3}\)5245\(\overline{0}\) NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (HUMAN);, mRNA sequence.
                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk,
                                                                           Unpublished
Emmert-Buck, M.D.,
                                                                                                                                                                                                                                                                         AI640146.1 GI:4703255
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                        ATTGAATCTTCAGCAGAATAATCCTTAAATATACTTTGTAAGCAAAACAAAAGCTTTTTT
                                                                                                                                                                              TCTCACTAATTTTAANAACTATTGAGAAAATTGATTAATGACATGAAGTGCACAACACTAA
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  ACTGAATCTTCAGCAGAATAATCCTTAAATATACTTTGTAAGCAAAACANAAGCTTTTNT
                                                                                                 TTACTGGCCAGCTGTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGGAAAACTCTTAA
                                                                                                                                                        TCTCACTAATTTTAAGAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACTAA
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                                                                             TTACTGGCCAGCTGTTGGCATTGTGTTTCTTACTTAGTTCTCCCAA-GGAAAACTCTTAA
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//clone lib="NCI GGAP_Kid11"
//note="Organ: kidney; Vector: pT773D-Pac (Pharmacia) with
/note="Organ: kidney; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
plasmid DNA from the normalized library NCI GGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 132376-132391, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo. "
96 a 128 c 114 g 278 t 5 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 9.4e-70;
0; Mismatches 21;
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ACCESSION
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Best Local Similarity
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770 bp mRNA linear EST 21-DEC-1999 wk33f07.x1 NCI CGAP Pr22 Homo sapiens cDNA clone IMAGE:2417221 3' similar to gb:$52450 NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (HUMAN);contains element MER28 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.B. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1454 Std Error: 0.00
Seg primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                  ATATCTCACTGAATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAA
                                                                                                         GCCAGAAAAAGTTATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCT
, ATATCTCACTGAATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 404.
Location/Qualifiers
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                         /lab host="pH108" // Clone lib="NCI CGAP Pr22" // Clone lib="NCI CGAP Pr22" // Clone lib="NCI CGAP Pr22" // Note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) // Note modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - Oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo. "71 a 111 c 99 g 285 t 4 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2417221"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="normal prostate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="male"
                                                                                                                                                                                    93.9%;
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Primates;
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                                                                                                                                                                 Score 670.4; DB 9;
Pred. No. 1.4e-69;
0; Mismatches 14;
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                            CCAGACCATAATTACCATATTAACTTTGTTNTGCACAGTTGTTTGCCAATTC 713
                                                                  GTTTACATAGTTCTTT-GGATTNTACTGTTCCTAATTTTATTCTGAAACTCAATTTTACC
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RESULT 5 BM985376 LOCUS KEYWORDS SOURCE ORGANISM REFERENCE VERSION ACCESSION DEFINITION JOURNAL MEDLINE TITLE AUTHORS discovery Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two appr Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 756) Homo sapiens

BM985376 756 bp mRNA linear UI-CF-EC1-acg-p-23-0-UI.sl UI-CF-EC1 Homo sapiens UI-CF-EC1-acg-p-23-0-UI 3', mRNA sequence. Homo sapiens (human) EST BM985376.1 GI:19611803 BM985376 cDNA clone EST 20-FEB-2003

COMMENT

Genome Res. 6 97044477 Contact: Mc McCray Lab 8889548 McCray, (9), PΒ 791-806

approaches to facilitate

Euteleostomi;

University of Iowa 2024 University of : Tel: 319 356 4866 Fax: 319 356 7171 Iowa Med Labs, Iowa City, İΑ

Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research

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BASE COUNT
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The following repetitive elements were found in
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The following repetitive elements were found in this cDNA sequence: 316-342, ANT rich#Low_complexity (matched compliment) seq.primer: M13 FORWARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCAGATAATTAAACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATA 181
                                                                                                                   TGATTTGGGAANAAAATACTGTTTCTGATAGCATGAAATGCAAAATTTTTTAGATTTTTAA 421
                                                                                                                                                                                                                       AAAATATTTTTATTTTAAAAAATAAGCCTGTGTTCAAGCTCTGATCATATTTCTTTTATTT
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/lab_host="Philb (Life Technologies) (T1 phage resistant)"
/lab_host="Philb (Life Technologies) (T1 phage resistant)"
/lone_lib="U1-CF-EC1"
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TAG_SEQ=AAGTGCTTAC"
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/tissue_type="Lung"
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97.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
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UI-CF-EN1-aei-a-17-0-UI.sl UI-CF-EN1 Homo sapiens cDNA clone
UI-CF-EN1-aei-a-17-0-UI 3', mRNA sequence.
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The following repetitive elements were found in this cDNA sequence: 316-342, AT rich#Low_complexity (matched complir Seq.primer: M13 FORWARD
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2024 University of Iowa Med Labs, Iowa City,
Tel: 319 356 4866
Fax: 319 356 7171
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/dev_stage="Adult"
//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//clone_lib="UI-CF-EN1"
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AW052045 786 bp wx25e05.x1 NCI CGAP Kid11 Homo sa similar to gb: $52450 NONSPECIFIC (ḤUMAN);, mRNA sequence.
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TAG_LIB-UI-CF-EN1
TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS chr-F-crand
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IC LIPID-TRANSFER PROTEIN PRECURSOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Catarrhini; Hor
1 (bases 1 to 786)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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Seq primer: -40UP from Gibco
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Emmert-Buck, M.D., Ph.D.
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AW052045.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg,
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/clone lib="NCI CGAP Kidl1":
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 132376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo. "
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116 c 109 g
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Primates;
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BQ008197.1 GI:19733097
EST.
                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

The following repetitive elements were found in this CDNA

sequence: 319-345, AAT_rich#Low_complexity (matched compliment)

Seq primer: M13 FORWARD

POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 751)
1 (bases 1 to 751)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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/clone lib="NCI_CGAP_ED1"

/note="Organ: Left Pubic Bone; Vector: pT773-Pac

(Pharmacia) with a modified polylinker; Site_1: EcoR I;

Site_2: Not I; NCI_CGAP_ED1 is a normalized cDNA library

containing the following tissue(s): Chondrosarcoma cell

line CS5. The library was constructed according to Bonaldo

Lennon and Soares, Genome Research, 6:791-806, 1996.

First strand cDNA synthesis was primed with an oligo-dT

primer containing a Not I site. Double stranded cDNA was

ligated to an EcoR I adaptor, digested with Not I, and
                                                                                                                                                                                /mol_type="mkNA"
/db xref="taxon:9606"
/clone="IMAGE:5836866"
/tl8sue_type="Chondrosarcoma"
                                                                                                                                                              /dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                            /organism="Homo sapiens
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                            Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 26-MAR-2002
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                BU619112
759 bp mRNA linear EST 23-SEP-2002
UI-H-FH1-bfm-l-10-0-UI.81 NCI CGAP FH1 Homo sapiens cDNA clone
UI-H-FH1-bfm-l-10-0-UI 3', mRNA sequence.
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BU619112.1 GI:23285327
EST.
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    sapiens (human)
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2 GCCAGAAAAAGTTAITTTAAITTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCT
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TAG_TISSUE=chondrosarcoma
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Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 316-342, >AT rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
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Mammalia; Eutheria;
1 (bases 1 to 759)
                                                                                                                                                                                                                                                                                                                            Similarity
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                             AATTGAAATGAGATTATAATTTGAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATTA 241
                                                                                                    TGCAGATAATTAAACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATA 181
                                                                                                                                                                                      ATATCTCACTGAATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAA 121
                                                                                                                                                                                                                                                       GCCAGAAAAAGTTATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCT
                                                                                                                                                     ATATCTCACTGAATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAA
                                                                                                                                                                                                                             GCCAGAAAAAGTTATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a cell line derived from grade I CHONGULVERLOWNE CONTROLL THE BOARD AND THE LIBRARY WAS CONSTRUCTED AND NORMALIZED ACCORDING to BONALDO, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is sequence tag for this library is AGAATCCGGC. The cell line was provided by Dr. James Martin from the University of
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Cell Line"
/dev_stage="Adult"
/lab_host="DH108 (Life Technologies)"
/clone_lib="NCI_CGAP_FH1"
/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not_1; NCI_CGAP_FH1 is a normalized cDNA library obtained from a cell line derived from grade I chondrosarcoma tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG_LIB=UI-H-FH1
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/db_xref="taxon:9606"
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Primates; Catarrhini; Hominidae;
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CCAGACCATAATTACCATATTAACTTTGTAATGCACAGTTGTATGC
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The following repetitive elements were found in this cDNA sequence: 315-341, APT rich#Low_complexity (matched compliment) Seq primer: M13 FORWARD Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Clone Distribution: Researchers may obtain clones from Research Seq primer: M13 POLYA=Yes. 2024 University of Iowa Med Labs, Iowa Tel: 319 356 4866 Fax: 319 356 7171 Genome Res. 6 (9), 791-806 (1996) 97044477 Eukaryota; Metazoa; Chordata; Craniata; Mammalia; Eutheria; Primates; Catarrhin 1 (base 1 to 721)
Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr Homo sapiens BM968746 721 bp mRNA linear EST 20-F) UI-CF-DU1-aam-a-03-0-UI.sl UI-CF-DU1 Homo sapiens cDNA clone UI-CF-DU1-aam-a-03-0-UI 3', mRNA sequence. Genetics (www.resgen.com) or from Open Biosystems University of Iowa McCray Lab Contact: McCray, BM968746.1 Homo sapiens (human) www.openbiosystems.com). 1. .721 /organism="Homo sapiens" Location/Qualifiers PB Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. mRNA approaches City, ΙÄ ţ facilitate gene EST 20-FEB-2003

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Query Match
Best Local Similarity
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TAG_LIB-UI-CF-DUI

TAG_TISSUE-Lung Epithelial Cells Tissue nos 359-368

TAG_SEQ-GGCTGTAGGC"

97 c 91 g 276 t
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/dev gtage="Adult"
/lab host="DH10B (Life Technologies) (T1 pha
/clome_lib="UI-CF-DUI"
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/db_xref="taxon:9606"
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Tissue Procurement: James Martin

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, University of Iowa
the following repetitive elements were found in this cDNA
sequence: 1-48, AT rich#Low complexity (matched compliment)
314-340, AT rich#Low complexity (matched compliment)
Seq primer: Mil FORWARD
POLYA=Yes.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 734)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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UI-H-FE1-bdv-m-12-0-UI.s1 NCI_CGAP_FE1 Homo sapiens cDNA clone
UI-H-E1-bdv-m-12-0-UI 3', mRNA sequence.
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CA424156.1 GI:24786882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                              261
                                                                                                                                                                                                                                                                        /clone lib="NCI CGAP FEI"
//clone lib="NCI CGAP FEI"
//clone "Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia / note="Organ: Chondrosarcoma; Site_1: EcoR I; Site_2: Not I; NCI CGAP FEI is a normalized cDNA library derived from a pool of mRNA obtained from 3 cell lines from grade II chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCTACGAC. The cell
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                                                                                                                                                                   TAG_LIB=UI-H-FE1
TAG_TISSUE=Human grade 2 chondrosarcoma cell line pool
                                                                                                                                                                                                                                                      lines were provided by Dr James Martin from the University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B_(Life_Technologies)"
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/db_xref="taxon:9606"
/clone="UI-H-FE1-bdv-m-12-0-UI"
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                       Score 663.2;
Pred. No. 1e-68;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
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Mammalia; Eutheria;
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762 bp mRNA linear EST 23-SEP-20 UI-H-FG0-bct-i-12-0-UI.51 NCI CGAP ENI 2 Homo sapiens cDNA clone UI-H-FG0-bct-i-12-0-UI 3', mRNA sequence.
BU627147
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National Cancer Institute, Cancer Genome Anat
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Pocas

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from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-43, -AT_rich#Low_complexity (matched compliment)
309-335, -AT_rich#Low_complexity (matched compliment)
Seq_primer: M13 FORWARD
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AATTTTAAGAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACTAATTACTGG
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                                                                                                                     GGAAGAAAATACTGTTTCTGATAGCATGAAATGCAAAATTTTTTAGATTTTTAATCTCACT
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TAG_INSUE=Enchondroma cell line (Mix of EN1 and EN2)
TAG_SEQ=CGGTCACTC"

TAG_SEQ=CGGTCACTC"

109 c 97 g 286 t 1 others
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/lab_host="DH10B (Life Technologies)"
/lab_host="NCI CGAP_EN1_2"
/clone_lib="NCI CGAP_EN1_2"
/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_EN1_2 is a cDNA library containing the following tissue(s): Enchandroma cell line (2 cell lines). The
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tissue_type="Enchondroma cell
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/db_xref="taxon:9606"
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Pred. No. 1.6e-68;
D; Mismatches 10;
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plate: LLCM2985 row: f column: 06
High quality sequence stop: 526.
Location/Qualifiers
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AGENCOURT 10507105 NIH MGC 127 H
IMAGE:6698694 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAGTTCTTTGGGATTTTTACTGTTCCTAATTTTATTCTGAAACTCAATTTTTACCCCAGACC
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                                                         /tissue types:mixed (pool of 40 RNAs)"
/tissue types:mixed (pool of 40 RNAs)"
/clone_lib="NHHOB(T1-phage-resistant)"
/clone_lib="NHH MGC_127"
/note="Vector: pDNR-LIB; Site_1: Sfil (ggccattatggcc);
Site_2: Sfil (ggccgcctcggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidnney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
used in cloning as follows:
5'-AAGCAGTGGTATCAACGCAAGTGGGCCATTACGGCCGGG-3' and
5'-ATTCTAGAGGCCGAGAGTGGCCACATG-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 1-2 kb
size fraction (other fractions present in NIH MGC 126 and
NIH MGC 128). Library created in the laboratory of T.
Usdīn, M.D., ph.D. (NIMH, NIH). Note: this is a NIH_MGC
                                   Library.
                                                                                                                                                                                                                                                                                                                                                                                                                             mol_type="mRNA"
db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96
Unpublished Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: James Martin
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 712)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                              BU619082.1 GI:23285297

BU619082

712 bp mRNA linear UI-H-FH1-bfm-f-06-0-UI.81 NCI CGAP FH1 Homo sapiens UI-H-FH1-bfm-f-06-0-UI 3', mRNA sequence.

BU619082
BU619082.1 GI:23285297
EST.
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                           Homo sapiens (human)
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Pred. No. 2e-68;
0; Mismatches
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2 GCCAGAAAAAGTTATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCT
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                             GTTTACATAGTTCTTTGGGATTTTTACTGTTCCTAATTTTATTCTGAAACTCAATTTTTACC
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                                                                                                 ACTGAATCTTCAGCAGAATAATCCTTAAATATACTTTGTAAGCAAAAACAAAAGCTTTTTT
                                                                                                                            ATTGAATCTTCAGCAGAATAATCCTTTAAATATATCTTTGTAAGCAAAACAAAAGCTTTTTT
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                                                                                                                                                                                                      TTACTGGCCAGCTGTTGGCATTGTGTTTCTTACTTAGTTCTCCCAA-GGAAAACTCTTAA
                                                                                                                                                                                                                                                                                                       TCTCACTAATTTTAAGAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACTAA
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BASE COUNT
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The following repetitive elements were found in this cDNA
sequence: 1-32, >AT_rich#Low_complexity (matched compliment)
298-324, >AT_rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arzayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained
NAAAATACTGTTTCTGATAGCATGAAATGCAAAATTTTTAGATTTTTAATCTCACTAATT
                                                                                                                               ATTTTAAAAATAAGCCTGTGTTCAAGCTCTGATCATATTTCTTTTATTTTGATTTGGGAA 372
                                                                                                                                                                                                                                                                                                                      GATTATAATTTGAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATTATTCTTAATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAATGCAGATAATT
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/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia ) with a modified polylinker; Site 1: EGGR I; Site 2: Not I; NCI CGAP FHI is a normalized cDNA library obtained from a cell line derived from grade I chondrosarcoma tissue. The library was constructed and normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAATCCGGC. The cell line was provided by Dr. James Martin from the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chondrosarcoma
TAG_SEQ=AGAATCCGGC"
99 c 89 g
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/tissue_type="Cell Line"
/dev_stage="Adult"
/lab_host="DH10B_(Life_Technologies)"
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97.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iow

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

The following repetitive elements were found in this cDNA

sequence: 316-342, >AT rich#Low_complexity (matched compliment)
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13 FORWARD POLYA=Yes.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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/lab host="MICI_CGAP_ED1"
/clone_lib="NCI_CGAP_ED1"
/clone_lib="NCI_CGAP_ED1"
/note="organ: Left Pubic Bone; Vector: pT7T3-Pac
/note="organ: Left Pubic Bone; Vector: pT7T3-Pac
/note="organ: Left Pubic Bone; Vector: pT7T3-Pac
/note="organ: Left Pubic Bone; Vector: Site_1: EcoR I;
Site_2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line CS5. The library was constructed according to Bonaldo
/Lennon and Soares, Genome Research, 6:791-806, 1996.
/Lennon and Soares, Genome Research, 6:791-806, 1996.
/First strand CDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="Chondrosarcoma"
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BASE COUNT
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Best Local Similarity 97.1%;
Matches 692; Conservative
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TAG_LIB=UI-H-EDI
TAG_TISSUE=chondrosarcoma
TAG_SEQ=CGTCAAGGCT"

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule, and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides mucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 258 A; 100 C; 92 G; 260 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gure
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Scanlan MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 710; DB 20; 1; Pred. No. 1.8e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Obata Y, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Old LJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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RESULT 2
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XX AAH575
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KW Human;
KW Lung;
KW Lung;
KW Long;
KW NO2001
XX D10-MAY
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                                                                                                                                                                                                                                                                                                                                              sequences (I). (I) can have cytostatic, immunomodulatory and concerning the content of the conte
                                                                                                  Query Match
Best Local Sin
Matches 700;
                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
metabolic disease; developmental disease; cytostatic; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH57161 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-291057/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sornasse T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-NOV-2000;
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                                                                                                                                    Similarity
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GCCAGAAAAAGTTATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCT
                                                                                                                                                                                                                                                  2663 BP; 807 A; 472 C; 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 258-259; 327pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; cDNA;
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                                                                                                                                 94.5%;
98.3%;
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                                                                                                      Pred. No. 2.3
0; Mismatches
                                                                                                                                    Score 674.4; DB 22;
Pred. No. 2.3e-107;
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                                                                                                                                                                                                                                                  G; 785 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gastric
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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
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Pfreundschuh
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                                                                                                Query Match
Best Local Similarity
Matches 480; Conser
                                                                                                                                                                                                                                                              The invention relates to a human colon tumour expressed polynucleotide (I) encoding a polypeptide (II, ABB67991-ABB97996) comprising; (i) any of 2600 fully defined nucleotide sequences (ABV8669-ABV89289); (ii) complements of (i); (iii) at least 20 contiguous residues of (i); (iv) sequences that hybridize to (i), under moderately stringent conditions; (v) sequences having at least 75% or 30% identity to (i); or (vi) degenerate variants of (i). The compositions and methods of the present invention are useful for the diagnosis, prevention and/or treatment of cancer, particularly colon cancer. (I) can be used in gene therapy and (I) and (II) are useful in pharmaceutical compositions such as vaccines. Note: The sequence data for this patent did not form part of the printed as pecification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated tumor colon polynucleotide and polypeptide, useful for the diagnosis, prevention and/or treatment of cancer, in particular colon cancer \cdot
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06-FEB-2001; 2001US-267011P.
28-MAR-2001; 2001US-279670P.
10-JUL-2001; 2001US-304037P.
                                                                                                                                                                                                 Sequence 486
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10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
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97US-0061765.
97US-0948705.
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New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products
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Best Local
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                                                                                                                                                                                                                                                         A single-stranded DNA (or its complementary strand or the corresp. CC double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of thuman genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) cc sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the GS '-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented CDNA hybridise with specific mRNAs. Each library CG is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be cequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                            Matches
                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene signature; messenger RNA; mRNA; relative abundance; human; cloning; mapping; non-biased library; diagnosis; d cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                               347
                                                                                     61
                                                                                                                                                                            337;
                                                                                                                                               N
                                                                                                                                                                                        Similarity
                  ATGCAGATAATTAAACTTACATGAAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTAT 180
                                                                                                                                 GCCAGAAAAAGTTATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTAT-CC
                                                                         TATATCTCACTGAATTTTAAGAAATAACATTAGTATTAGAAAAAACTAGGAAAAAAAGATAA
                                                                                                                  GCCAGAAAAGTTATTTTAATTTCCTATTAAACATNCTCCTCAAAGCATTATTTTANCCC
                                                                                                                                                                          Conservative
                                                                                                                                                                                      43.9%;
                                                                                                                                                                         0
                                                                                                                                                                                      Score 313.2; DB 16; Pred. No. 2.7e-45;
                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                 141 T; 5 other;
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RESULT 7
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                                                                                                                                                           CC AAH57161 to AAH57576 represent cell and tissue specific polymucleotide CC sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and CC neuroprotective activities, and can be used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and CC pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from CC differentiation of embryonic stem cells into a tissue selected from CC tissues. (I) and (II) are used to produce an expression profile that CC disease or disorder. The gene profile can be used for diagnosis, composis or monitoring of treatments and for investigating a CC predisposition to a disorder where the gene is associated with a CC cancer, immunopathology or neuropathology.
  Best Loc
Matches
                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-NOV-2000; 2000WO-US30396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
metabolic disease; developmental disease; cytostatic; immunomodulatory;
neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human liver specific cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-2001
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                                Local
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                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 117; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAATATTT-TTATTTTAAAAATAAGCCTGTGTTCAAGCTCTGATC 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATTGAAATGAGATTATAATTTGAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTCTTAATGATGGTGTTTTATGACTAATACACTGATTTTTCAATAAGGAAACCCATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATTGAAATGAGATTATAATTTGAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAATATTTNTNNTTTTAAAAATAAGCCTGTGTTCAAGCTCTGATC 1
     Conservative
                                                                                                               B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seilhamer JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specific; diagnosis; brain; heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9908-0163508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA;
                             36.2%;
98.9%;
                                                                                                               ð
                                                                                                               38 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262
     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watson GA;
                             Score 258.4;
Pred. No. 7.1
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                                                                                                               34 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:133
                                                                                                               87
                                                                                                               Ţ,
                             .1e-36;
                                                                                                            0 other,
                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      skeletal muscle;
     Indels
                                                       Length
                                                       262;
  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene is
Gaps
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RESULT 8
ABX83093/c
ID ABX83093;
XX ABX83093;
XX ABX83093;
XX ABX83093;
XX ABX83093;
XX ABX83093;
XX Corn ear-c
CC Corn-car
CC Corn-ear-c
CC arcar ear-c
CC arcar
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The present invention relates to the isolation of corn ear-derived polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMONO23 and SATMONO23. Some of the cpds uniquely identify structural, functional, and regulatory genes of corn ear. The polynucleotides sequences are useful for detecting cpds in a sample, for producing a corn ear-specific profile of gene transcription, for detecting altered gene expression in inbred or hybrid plants, and for screening several molecules for specific binding to the polynucleotide. The cdps are useful to identify, isolate, or extend identical or related corn-ear nucleic acid sequences from DNA libraries, and in nucleic acid amplification or hybridisation techniques to follow the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel purified corn-ear derived polynucleotide useful as hybridization probe for detecting polynucleotide in sample, and for identifying, evaluating, and altering desired characteristics associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               corn ear-specific profile; gene transcription; gene expression; hybrid plant; desirable trait expression; plant breeding prograinheritance; desired characteristic; growth; development; disease resistance; environmental adaptabilition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lalgudi RV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease resistance; environmental adaptability; quality;
multigene trait; plant; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corn ear-derived polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ear-derived polynucleotide; cdp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; cDNA; 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAAAAATAAGCCTGTGTTCAAGCTCTGATCATATTTCTTTTATTTTGATTTGGGAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAAAAATAAGCCTGTGTTCAAGCTCTGATCATATTTCTTTTATTTTGATTTGGGAANAAA 376
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                                                                                                                                                                                                                                                                                                                                                                                          SEQ
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                                                                                                                                                                                                                                                                                                                                                                                          No 1553;
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                                                                                                                                                                                                                                                                                                                                                                                       390pp; English.
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RRESULT 9
ABX4079
ID ABX44
XX ABX44
XX BOV1
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XX Gene
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Best Local Similarity 97.7
Matches 168, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression of desirable traits through plant breeding programs. Preferably, the cdps are used to identify, evaluate, alter, or follow the inheritance of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality, and yield of corn. The cdps are also useful as molecular markers for studying inheritance and multigene traits in a plant breeding program. The cpds are useful for producing purified corn-ear polypeptides by recombinant techniques. They are also useful in diagnostic assays to detect or confirm conditions or diseases associated with abnormal levels of cdp expression. ABX81541-ABX89140 represent corn ear-derived polynucleotides (cpds) of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                    New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine; 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 173
Claim 2; SEQ ID No 5962; 245pp; English
                                                                                                                                                                                 WPI; 2003-110599/10
                                                                                                                                                                                                                                            Byatt JC,
                                                                                                                                                                                                                                                                                                    (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
(TAON/) TAO N.
(WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JAN-1999; 99US-115707P.
11-JAN-2000; 2000US-0480902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-SEP-2001; 2001US-0960352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos Taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine EST associated with lactation/muscle/fat deposition #5962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACTGAATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAATGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACTGAATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAATGCAGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAAGTTATTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCTATATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAGTTATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCTATATCT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAATTAAACTTACATGAAAAAGGAAATTATAACAAAGGACTGAGAACGTTA 1
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                                                                                                                                                                                                                                      Mathialagan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cattle breeding
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97.7%;
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Pred. No. 6.2e-20;
0; Mismatches 4
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The invention relates to a purified nucleic acid molecule associated with CC lactation or muscle and fat deposition (designated LMPD), derived CC from cattle, and the LMPD nucleic acid can specifically hybridise to a Second nucleic acid molecule comprising any of 15112 nucleotide CC sequences, appearing as ABX34836-ABX49947, or complements of them. CC Also included are; (1) a transformed cell having a nucleic acid comprising an IMPD nucleic acid linked to a promoter and 3; non-cc translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3; end confidence in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule complement or fragment) with a complementary nucleic acid molecule complement or fragment) with a complementary nucleic acid molecule complementary nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detection of the level or pattern of the complementary nucleic acid is used for detection of the complementary nucleic acid is used for detection of the complementary nucleic acid is used for detection of the molecule. The LMPD nucleic acid is used for detection of the molecule. The present sequence is one of the 15112 bovine complementary actile. The present sequence is one of the 15112 bovine complements used of the complementary of the lavel or pattern of the molecule. The present sequence is one of the 15112 bovine complements used of the complement of the specification but was obtained in abovine cased not shown in the specification but was obtained in electronic format from the USPTO web site:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seqdata.uspto.gov/sequence.html?DocID=20020137139.
                                             675
                                                                                         181
                                                                                                                                      615
                                                                                                                                                                                    125
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                                                                                                                                                                                                               CAGAATAATCCTTAAATATACTTTGTAAGCAAAAACAAAAGCTTTTTTTGTTTACATAGTTC
                                                                                                                                                                                                                                                                             AATAATGATAT-TCTGTTTCTTCATTCTCCCAAGGAAAAC----TTGAAATTTCGG 124
                                                                                                                                                                                                                                                                                                          GTTGGCATTGTGTTTCTTACTTAGTTCTCCCCAAGGGAAAACTCTTAAATTGAATCTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                      AANAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACTAATTACTGGCCAGCT
                        ACCATATTAACTTTGTTNTGCACAGTTGTTTGCCAAT
                                                                                                                     TTTGGGATTTTACTGCTAATTTTATTCTGAAACTCAATTTTACCCCCAGACCATAATT
                                                                                                                                                                                    CAGAATAATCTTCAAATATACATTATTAGCAAAATGAGAGCTTCTGTTT----ACATACT 180
                                                                                                                                                                                                                                                                                                                                                                      TTTTGTATTTTGCTATTTCTAACTTTATTCTAAAACTCAATTTTACCCCCAAACCATGATT
ACCATATTAACTTTGTAATGCACAGTTGTTTGCAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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73.6%;
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Pred. No. 3.7e-13;
0; Mismatches 60
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RESULT 10
AAQ76489/c
ID AAQ76489 standard; DNA; 263 BP.

XX
AC AAQ76489;
XX
PT 25-MAR-2003 (updated)
DT 23-SEP-1994 (first entry)
XX
DE Human genome fragment.
XX
XX
KW Brain; placenta; bone marrow; genetic analysis; gene mapping;
XX
KW detection; homology; human; adrenal tissue; ds.
XX
PN W09401548-A2.
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RESULT 11
ABZ10246
ID ABZ110246
AC ABZ110
AC ABZ110
AC ABZ11
AC AB
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                                                                                                                                                                                                                                      Haematopoietic cell proliferation disorder related DNA sequence #386.
                                                                                                                                                       cytosine methylation
                                                                                                                                                                                                Human; haematopoietic cell proliferation disorder; cytostatic;
                                                                                                                                                                                                                                                                                           16-JAN-2003
                                                                 WO200277272-A2
                                                                                                                                                                                                                                                                                                                                                                               ABZ10246 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human nucleic acid fragments, isolated from brain adrenal tissue, the placenta or bone marrow comprise any of: (A) a sequence selected from (AAQ76401-Q77613), (B) an allelic variation of a sequence as described in (A), or (C) a sequence complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-035056/04
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                                                                                                          sapiens
                                                                                                                                                                            therapy;
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82.1%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CGG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells and proliferative consociations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG
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                                      10.9%;
nilarity 47.3%;
Conservative
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Pred. No. 7.9e-05;
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences, appearing as ABXJ4836-ABX49947, or complements of them. Also included are; (1) a transformed call having an nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that functions in the cell to cause termination of
                                                                                                                                               Claim 2;
                                                                                                                                                                        New nucleic acid associated with lactation, and muscle and deposition, useful for genome mapping, gene identification analysis, cattle breeding, or for genetically improving cat
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ABX48095/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC transcription and addition of polyadenylated ribonucleotides to a 3' end CC of the mRNA molecule; and (2) determining a level or pattern of a CC molecule in a bovine cell or tissue comprising: (a) incubating a marker CC nucleic acid (comprising any of the 15112 nucleic acid sequences or its CC obtained from the bovine cell or tissue, where hybridisation between the CC marker nucleic acid and the complementary nucleic acid permits the CC marker nucleic acid and the complementary nucleic acid permits the CC complementary nucleic acid, where the detection of the molecule; and (b) detecting the level or pattern of the CC complementary nucleic acid, where the detection of the complementary cC complementary nucleic acid, where the detection of the molecule. The LMFD nucleic acid is used for determining a level or pattern of the CC mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genecically constructs for use in cattle gene expression, or for genecically constructs for use in cattle gene expression, or for genecically constructs for use in cattle gene expression, or for genecically constructs for use in cattle gene expression, or for genecically constructs for use in cattle gene expression, or for genecically constructs for use in cattle gene expression, or for genecically constructs for use in cattle gene expression, or for genecically constructs are not sequence is one of the 15112 bovine constructs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 120;
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Best Local
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                                                                                              (BYAT/)
(MATH/)
(TAON/)
                                                                                                                                                                                                                                                                                                                                                                 Bovine; ss; EST; expressed sequence tag; lactation; muscle deposition; fat deposition; genome mapping; ;
                                             Byatt JC,
                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine EST
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             WPI; 2003-110599/10
                                                                                                                                                                12-JAN-1999;
11-JAN-2000;
                                                                                                                                                                                                                24-SEP-2001; 2001US-0960352.
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                                                                                WARR/)
                                                                                                                                                                                                                                                                                                                                                   analysis;
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                                                                                              BYATT J C.

MATHIALAGAN

TAO N.
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                                                                              WARREN W C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                                             Mathialagan
                                                                                                                                                                                                                                                                                                                                                                                                                    associated with
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                                                                                                                                                                 99US-115707P.
2000US-0480902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                   cattle breeding
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76.4%;
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Pred. No. 0.00011;
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RESULT 14
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CC sequences, appearing as ABX34816-ABX349347, or complements of them.
CC Also included are; (1) a transformed cell having a nucleic acid
CC comprising an LMFD nucleic acid linked to a promoter and a 3' non-
CC translated sequence that functions in the cell to cause termination of
CC transcription and addition of polyadenylated ribonucleotides to a 3' end
CC of the mRNA molecule; and (2) determining a level or pattern of a
CC molecule in a bovine cell or tissue comprising: (a) incubating a marker
CC nucleic acid (comprising any of the 15112 nucleic acid sequences or its
CC complement or fragment) with a complementary nucleic acid molecule
CC marker nucleic acid and the complementary nucleic acid molecule
CC marker nucleic acid and the complementary nucleic acid molecule
CC marker nucleic acid and the complementary nucleic acid molecule
CC complementary nucleic acid, where the detection of the complementary
CC nucleic acid is predictive of the level or pattern of the
CC complementary nucleic acid is used for determining a level or pattern
CC nucleic acid is used for determining a level or pettern
CC mapping, gene identification and analysis, cattle breeding, preparation
CC improving cattle. The present sequence is one of the 15112 bovine
CC LMFD EST (expressed sequence tag) nucleic acid.
CC CMFD EST (expressed sequence tag) nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse ischaemic condition related cDNA sequence SEQ ID NO:842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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          (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; SEQ ID No 13260; 245pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D EST (expressed sequence tag) nucleic acids.

e: The present sequence was not shown in the specification but obtained in electronic format from the USPTO web site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              compressive ischaemia; occlusive ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                              ischaemic
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                          condition;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.00022;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB19914
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Examining the ischemic condition (e.g. expression levels of particular genes of by determining the expression profile c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   are used
                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 2152
                                                                                        TTGTTTACATAGTTCTTTGGGATTTTACTGTTCCTAATTTTTATTCTGAAACTCAA-TTTT 658
ACCCCAAACCATCATTGACATAGTCAGCTT 1883
                            ACCCCAGACCATAATTACCATATTAACTTT
                                                                ---GTTTACTCAGTCTTCAGATTTTACTAGTTCTGAATTTTATTCTGAAACTCAAGTTTA 1913
                                                                                                                                     ACACCGAGTGTCCAACACAGTGATCCTCAAATATAC
                                                                                                                                                              AAATTGAATCTTCAGCAGAATAATCCTTAAATATACTTTGTAAGCAAAACAAAAGCTTTT
                                                                                                                                                                                                       AATTCCTGGTCAACT-ATGGAAATCTGTTTCTTCTAGTCCCCCCAAGGAGAAA-TGTC
                                                                                                                                                                                                                                      AATTACTGGCCAGCTGTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGGAAAACTCTT
                                                                                                                                                                                                                                                                          AATTTTATTTTAAGGAACTATTAGTGAGAAACTGATGCAGGTAATTGAGTGTGAGGCACT
                                                                                                                                                                                                                                                                                                          AATCTCACTAATTTTAANAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 2087-2091; 2690pp;
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asai S,
                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                               primers for a mouse ischaemic condition related sequence, in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                 586 A; 455 C;
                                                                                                                                                                                                                                                                                                                                                            10.3%;
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Pred. No. 0.00045;
                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 576 G; 535 T; 0 other;
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                                688
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RESULT 15
ABZ10246/c
ID ABZ10246;

XX
AC ABZ10246;

XX
DT 16-JAN-2003 (first entry)

XX
DE Haematopoietic cell proliferation disorder related DNA sequence #386

XX
Equation therapy; lymphocytic leukaemia, acute myelogenous leukaemia;

XX
Cytosine methylation state; gene; ds.

XX
PN
W0200277272-A2.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for detecting and differentiating between haematopoletic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated cpd dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lewin A,
Pelet C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder
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Piepenbrock C, Adorjan P, Grabs
Lipscher E, Maier S, Model F,
Schwope I, Ziebarth H;
TACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAAATTGAAATGAGATTA 197
                                                                                               TAATTTGAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATTATNCTTAATGATGGTGT
                                                                                                                                                                                                                                                                                                                                          TAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAATGCAGATAATTAAACT 137
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e R, Leu E;
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111:	1170 TCAAAAATATAATTTTAAATTTTCAAATATCAAAAAAAA	1170	В
551	492 GCTGTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGGAAAACTCTTTAAATTTGAATCTT 551	492	Ş
117:	1230 TTTTATTATAAAAAAATTAAATTAAATAATATTAAAATTTAAAA	1230	pb
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123:	1290 ATATTACATTTTTATATATTATATATATTACATAACATTTTTT	1290	8
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Search completed: November 27, 2003, 06:23:42 Job time: 236.619 secs

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seq length: 2000000000
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1: /cgn2_6/ptcodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptcodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptcodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptcodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptcodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptcodata/1/pubpna/US07_NEW_PUB.seq:*

7: /cgn2_6/ptcodata/1/pubpna/US08_NEW_PUB.seq:*

9: /cgn2_6/ptcodata/1/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptcodata/1/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptcodata/1/pubpna/US09_PUBCOMB.seq:*

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13: /cgn2_6/ptcodata/1/pubpna/US09_NEW_PUB.seq:*

14: /cgn2_6/ptcodata/1/pubpna/US10A_PUBCOMB.seq:*

15: /cgn2_6/ptcodata/1/pubpna/US10A_PUBCOMB.seq:*

16: /cgn2_6/ptcodata/1/pubpna/US10A_PUBCOMB.seq:*

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17: /cgn2_6/ptcodata/1/pubpna/US10A_PUB.seq:*

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9 US-09-835-992A-20
10 US-09-96-692-7228
11 US-10-040-862-7228
12 US-09-98-598-598-522
14 US-09-985-992A-22
14 US-01-102-524-161
14 US-10-102-524-188
14 US-10-9-960-352-13016
15 US-09-960-352-13016
16 US-09-960-352-13016
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Sequence 19, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 7228, Ap
Sequence 7228, Ap
Sequence 578, App
Sequence 161, Appl
Sequence 188, App
Sequence 645, App
Sequence 6962, Ap
Sequence 13016, A
Sequence 13016, A
Sequence 13260, A
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
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ALIGNMENTS

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57.6	57.6	57.6	57.8	57.8	82	58.2	58.4	58.4	58.4	58.4	58.6	58.8	59.2	59.4	59.4	59.6	59.6	60.6	60.8	61.4	61.4	61.8	62	62.2	63.6	64.6	65.2	65.2
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US-10-311-455-1855	US-10-311-455-1114	10-074-	US-10-311-455-1933	US-10-198-846-1369	US-10-312-841-2	US-09-790-988-1	US-10-311-455-2148	US-10-240-485-90	US-10-311-455-1064	US-10-311-455-2405	US-09-960-352-5301	US-10-311-455-2147	US-10-311-455-2090	US-10-240-453-210	US-10-311-455-1916	US-10-311-455-834	US-10-240-453-245	US-10-240-453-327	US-09-960-352-11218	US-10-312-841-1	US-10-311-455-1702	US-10-311-455-1260	US-10-312-841-2	US-09-960-352-13694	US-10-172-086-111	US-10-311-455-1445	US-10-312-841-1	US-10-240-485-151
Sequence 1855, Ap	1114	Sequence 60, Appl	Sequence 1933, Ap	Sequence 1369, Ap	e 2	Sequence 1, Appli	Sequence 2148, Ap	90	10	Sequence 2405, Ap	53	21	20	21	19	83	24	32	Sequence 11218, A	Sequence 1, Appli	Sequence 1702, Ap	Sequence 1260, Ap	Sequence 2, Appli	Sequence 13694, A	Sequence 111, App	Sequence 1445, Ap	Sequence 1, Appli	Sequence 151, App

US-09-835-992A-19 iSequence 19, Application US/09835992A Patent No. US20020037541A1 GENERAL INFORMATION: APPLICANT: Obata, Yuichi TITLE OF INVENTION: NOTATED NUCLEIC ACID MOLECULES ASSOCIATED WITH GASTRIC CANCER AN. TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING GASTRIC CANCER AN. TITLE REFERENCE: L0461/7112 CURRENT FILING DATE: 2001-04-16 PRIOR APPLICATION NUMBER: US/09/835,992A CURRENT FILING DATE: 2001-04-16 PRIOR APPLICATION NUMBER: US 08/896,164 PRIOR APPLICATION SEGO ID NOS: 87 SOFTWARE: PatentIn version 3.0 SEQ ID NO 19 LENGTH: 714 TYPE: DNA ORGANISM: Homo sapiens NAME/KEY: Unsure LOCATION: (373)...(373) OTHER INFORMATION: n = a NAME/KEY: Unsure LOCATION: (437)...(437) OTHER INFORMATION: n = a NAME/KEY: Unsure LOCATION: (702)...(702) OTHER INFORMATION: n = a NAME/KEY: Unsure LOCATION: (702)...(702) OTHER INFORMATION: n = a US-09-835-992A-19 NAME/KEY: Unsure LOCATION: (243)...(243) OTHER INFORMATION: n = a, FEATURE: a a 'n ņ ņ ņ ņ ω ω Ø ω 9 õ õ õ

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1 CGCCAGAAAAGTTATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCC 60

Query Match Best Local Similarity Matches 714; Conserv

99.4%; Score 710; DB 9; Larity 100.0%; Pred. No. 7.9e-118; Conservative 0; Mismatches 0;

Length 714;

<u>,,</u>

Gaps

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APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR PILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                        Sequence 3296, Application Patent No. US20020142981A1 GENERAL INFORMATION:
                                                                SEQ ID NO 3296
LENGTH: 1052
FEATURE: OTHER INFORMATION: Genbank Accession
                                 ORGANISM: Homo sapiens
                                                   TYPE: DNA
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Sequence 20, Application US/09835992A

Patent No. US20020037541A1

Patent No. US20020037541A1

APPLICANT: Obata, Yuichi
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOI
TITLE OF INVENTION: METHODS FOR DIAGNOSING A
FILE REFERENCE: L0461/7112

CURRENT APPLICATION NUMBER: US/09/835,992A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 08/896,164
PRIOR FILING DATE: 1997-07-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
SEQ ID NO 20
LENGTH: 687
TYPE: DNA
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LOCATION: (541)..
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                                                                       ACCATA-TTAACTTTGTTNTGCACAGTTGTT
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GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: MAINTON, Jane
FILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION NUMBER: US/09/796,692
CURRENT FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILLING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,799
PRIOR APPLICATION NUMBER: 60/200,799
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/203,318
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR APPLICATIO
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; TYPE: DNA
; ORGANISM: Homo :
US-09-796-692-7228
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Similarity 99.2%;
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PRIOR FILING DATE: 2000-08-04
PRIOR PELICATION NUMBER: US 60/223,378
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7228
LENGTH: 506
TYPE: DNA
TYPE: DNA
TORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2000-01-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR PRILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
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US-10-040-862-7228
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Publication No. US20030078396A1
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
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                                                                                          ATATCTCACTGAATTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAA
                                                                                                                                  ATATCTCACTGAATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAA 121
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APPLICANT: Xu, Jiangchun
APPLICANT: Chemault, Ruth A.
APPLICANT: Chemault, Ruth A.
APPLICANT: Chemault, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SRO ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 578
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-578
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US-09-998-598-578
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED WITH GASTRIC CANCER TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING GASTRIC CANCER FILE REFERENCE; LO461/7112 CURRENT APPLICATION NUMBER: US/09/835,992A CURRENT FILING DATE: 2001-04-16 PRIOR APPLICATION NUMBER: US/08/896,164 PRIOR FILING DATE: 1997-07-17 NUMBER OF SEQ ID NOS: 87 NUMBER OF SEQ ID NOS: 87
                                                         LOCATION: (69)..(69)
OTHER INFORMATION: n
NAME/KEY: Ungure
LOCATION: (71)..(71)
OTHER INFORMATION: n
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LOCATION: (35)..(35)
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LOCATION: (12)..(12)
OTHER INFORMATION: n
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OTHER INFORMATION: n
NAME/KEY: Ungure
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US-10-102-524-161/c

Sequence 161, Application US/10102524

Publication No. US20030109434A1

GENERAL INFORMATION:

APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Galger, Alexander
APPLICANT: Gordon, Brian
APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCE
FILE REFERENCE: 20121.572

CURRENT APPLICATION UMMBER: US/10/102,524

CURRENT FILING DATE: 2002-03-19

NUMBER OF SEQ ID NOS: 1863

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 161

LENGTH: 510

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APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Gaiger, Alexander

APPLICANT: Gordon, Brian

APPLICANT: Gordon, Brian

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CAI

FILE REFERENCE: 210121.572

CURRENT APPLICATION NUMBER: US/10/102,524

CURRENT FILING DATE: 2002-03-19

NUMBER OF SEQ ID NOS: 1863

SOFTMARE: FASISEO for Windows Version 4.0

SEQ ID NO 188

LENGTH: S10

TYPE: DNA

ORGANISM: Homo sapiens

US-10-102-524-188
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US-10-102-524-645
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US-10-102-524-161
Sequence 645, Application US/10102524 Publication No. US20030109434A1 GENERAL INFORMATION:
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Publication No. US20030109434A1
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                                                                                                                                                                                                                                                                                                                     CTGTTGGCATTGTGTTTCTTACTTAGTTCTCCCAA-GGAAAACTCTTAAATTGAATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTACCATATTAACTTTGTAATGCACAGTTGTATGCAATTCC 292
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96.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 188; DB 14; Length 510; Pred. No. 1.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 188; DB 14;
Pred. No. 1.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF KIDNEY CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
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GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengbing

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

APPLICANT: Mathialagan, Nagappan

ITILE OF INVENTION: NUCCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

ITILE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT APPLICATION UNMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 5962

LENGTH: 397

TYPE: DNA

ORGANISM: Bos taurus

OTHER INFORMATION: Clone ID: 26-LIB188-014-Q1-E1-G5
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY
FILE REFERENCE: 210121.572
CURRENT APPLICATION NUMBER: US/10/102,524
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 1863
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 645
LENGTH: 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Algate, Paul A
APPLICANT: Mannion, Jane
APPLICANT: Gaiger, Alexa
APPLICANT: Gordon, Brian
APPLICANT: Harlocker, Su
                                                                                                                                                                     Query Match
Best Local Similarity
Matches 204; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match Best Local Similarity Matches 213; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5962, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         673 TTACCATATTAACTTTGTTNTGCACAGTTGTTTTGCCAATTC 713
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                        495 GTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGGAAAACTCTTAAATTTGAATCTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
74 AATAATGATAT-TCTGTTTCTTCATTCTCCCAAGGAAAAC---
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                                                                                                             AANAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACTAATTACTGGCCAGCT
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                                                                                     Mannion, Jane
Gaiger, Alexander
Gordon, Brian
                                                                                                                                                                          Conservative
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                                                                                                                                                                                       17.7%;
73.6%;
                                                                                                                                                                     Score 126.2; DB 10;
Pred. No. 1.8e-13;
D; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 188; DB 14;
Pred. No. 1.7e-24;
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                                                                                                                                                                          60; Indels 13;
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                                                                                                                                                                                                              Length 397;
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US-09-960-352-13260/c
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US-09-960-352-13016/c
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US-09-960-352-13260
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                                                                                      APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 13260
                                                                                                                                                                                                                                                                                                   Sequence 13260, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
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APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 13016
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
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         LENGTH: 449
TYPE; DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                            APPLICANT: Warren, Wesley C. APPLICANT: Tao, Nengbing APPLICANT: Byatt, John C. APPLICANT: Mathialagan, Nag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCATATTAACTTTGTTNTGCACAGTTGTTTGCCAAT 711
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                 Clone
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                 ID:
               57-BOVMS1-016-Q1-E1
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Pred. No. 0.00012;
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APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, ANI
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PRI
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
INUMBER OF SEG ID NOS: 14064
SOFTWARE: FASTSEQ for Windows Version 4.0
SOFTWARE: FASTSEQ for Windows Version 4.0
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US-10-198-846-6381/c
US-10-198-846-6381, Application US/10198846
; Publication No. US20030099974A1
                                                                                                                                                                                                                                                      US-10-198-846-6381
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Best Local Similarity 85.6
                                                                                                                                                                                      Matches
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Lillle, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kat
                                                                                                                                                                                                                                                                NAME/KBY: misc_feature
LOCATION: 807, 808, 819, 820, 821,
LOCATION: 871, 874, 875, 891, 892,
LOCATION: 917, 923, 925, 926, 927,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 428, 433, 450, 465, 466, LOCATION: 517, 518, 528, 530, 534, LOCATION: 590, 610, 625, 626, 642, LOCATION: 690, 700, 702, 706, 716, OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1, 8, 66, 71, 79, 81, 84,
LOCATION: 1149, 156, 162, 166, 172, 7
LOCATION: 268, 271, 273, 274, 275, 2
LOCATION: 359, 366, 374, 393, 404, 4
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 960
                                                                                                                                                                                   Local Similarity
les 217; Conserv
                    187
                                                                                                                                                     67
AAATGAGATTATAATTTGAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATTATNCTT
                                                 ĀŖĀTĪTĪTTNARĀRĀCTĀĀTTNTAĀNNĀTANTNĀATTTTTNTARĀRĀRANNNĀRĀRĀTTR
                                                                                  ATAATTAAACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAAATTG 186
                                                                                                                     TNANNNANACCTANACCTTTAAANATNTNNNANTTNAANNAAAAAAATATTTAAANNTAN 871
                                                                                                                                                  TCACTGAATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAATGCAG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCATATTAACTTTGTTNTGCACAGTTGTTTGCCAAT 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTGTATTTTGTTATTTCTAACTTTATTCTAAAACTCAATTTTACCCCAGACCATGATT
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                  9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.5%;
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                                                                                                                                                                                                  Score 67.6; DB 14;
Pred. No. 0.0073;
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Pred. No. 0.00025;
0; Mismatches 1:
                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179,
276,
406,
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APPLICANT: ZWIEBEL, LAURENCE J.

TITLE OF INVENTION: MOSQUITO OLFACTORY GENES, POLYPEPTIDES, AND METHODS OF

TITLE OF INVENTION: USE THEREOF

FILE REFERENCE: N7841

CURRENT APPLICATION NUMBER: US/10/056,405

CURRENT APPLICATION NUMBER: 60/264,649

PRIOR APPLICATION NUMBER: 60/264,649

PRIOR PILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 10

LENGTH: 4985

TYPE: DNA

ORGANISM: Anopheles gambiae

US-10-056-405-10
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US-10-056-405-10
US-10-056-405-10
Sequence 10, Application US/10056405
; Publication No. US20030166013A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.4%;
Best Local Similarity 44.4%;
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TAATTTTAANAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACTAATTACTG 487
                                                                                                                                                                                                                                          ATGATGGTGTTTTATGACTAATACACTGATTTTTCAAGAAGGAAACCCATGTTAAAAATA 307
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                                                                                            GGGAANAAATACTGTTTCTGATAGCATGAAATGCAAAATTTTTTAGATTTTTAATCTCAC 427
                                                                                                                                           TGATTTTTATTTTAAGAGAAAGATAAACCATTTTTAGTAACCAATTTAGTTACAGGAACC 2336
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Pred. No. 0.014;
0; Mismatches 325;
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Search completed: November 27, Job time: 275.238 secs 2003, 12:52:53

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfIles1.seq:*
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US-08-896-164-29
US-08-896-164-20
US-08-896-164-20
US-08-896-164-20
US-08-98-106-2
US-09-313-294A-553
US-09-313-001C-150
US-09-641-638-651
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US-08-998-416-186
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Sequence 20, Appl
Sequence 22, Appli
Sequence 251, App
Sequence 551, App
Sequence 150, App
Sequence 186, App
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GENERAL INFORMATION:
             APPLICATION NUMBER: US/08/
FILING DATE: July 17, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6218521man D. Ha
REGISTEATION NUMBER: 30,94
                                                                                                    COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                       ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           APPLICANT: OBATA, YUICHI
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES
TITLE OF INVENTION: WITH GASTRIC CANCER AND METHODS
TITLE OF INVENTION: DIAGNOSING AND TREATING GASTRIC
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             ; Sequence 22, Application; Patent No. 6218521; GENERAL INFORMATION: APPLICANT: OBATA, YUTITLE OF INVENTION:
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Best Local Similarity
Matches 671; Conserv
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 20:
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LENGTH: 687 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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APPLICATION DATA:
APPLICATION NUMBER: US/08/896.
FILING DATE: ULly 17, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6218521man D. Hansor
REGISTRATION NUMBER: JUD :
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 688-9200
TELEPAX: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LEVINGER CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 61.1%;
Best Local Similarity 73.1%;
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Diskette, 3.50 inch, 1.44mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOPTMANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 843 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                  TTACTGGCCAGCTGTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGGAAAACTCTTAA 541
                                                                       CCCCCCTANTTTTAAAANCTATNGAAAANTNGATTANNGACTTGAATTGC-CAACCCTAN
                                                                                                                                               GGATTGGGGAAAAAAATNCNGTTCCNNATACCNNGAANNGCAAANTTTTTAAATTTTTAA
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TTNCNGGCCACCNGTGGGCNTNGTNTTCCTTACTTANTCCCCCCAA-GGAAANNCCTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 436.2; DB 3;
pred. No. 4e-78;
0; Mismatches 187;
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US-09-313-294A-1553/c
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US-07-867-106-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SOFTWARE: PERL Prog
SEQ ID NO 1553
; LENGTH: 173
; TYPE: DNA
; ORGANISM: Zea mays
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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN:
FILE REPERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1553, Application US/09313294A Patent No. 6476212
                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/07867106 Patent No. 5389526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                     GENERAL INFORMATION:

APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 538957
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700551132H1
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                       STATE: P
                                                                                           CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 TAATTAAACTTACATGAAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTA 179
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Floppy disk
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97.7%;
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Pred. No. 9.7e-25;
0; Mismatches 4
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US-07-867-106-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 46.8 Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1992062 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
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NAME/KEY:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US
FILING DATE: 19920625
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                                                                                                                                                                                                                                                                                                                                                       5571
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5271 AATGGATACTAGATCCTTTTTCCCAAGTTTTCC 5239
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                                                                                                                                                                                                           5451 TTTTTAÄÄÄÄTTCÄAATAATTAAATAATTATCTATÄTÄTCTTGATGÄACTTCÄÄTTTTTÄ
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                                  492 GCTGTTGGCATTGTGTTTCTTACTTAGTTCTCC
                                                                                                    432 TTTAANAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACTAATTACTGGCCA
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2378..5038
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 5.3e-05;
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RESULT 6
US-09-641-638-651/c
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SEQ ID NO 651
*ENGTH: 20674
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CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
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                           NAME/KEY: exon
LOCATION: 16567..16667
OTHER INFORMATION: exon
NAME/KEY: exon
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NAME/KEY: misc_feature
LOCATION: 1123..3123
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INFORMATION: exon 13
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Chumakov, Ilya
Cohen, Annick
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NAME/KEY: allele
LOCATION: 5903
OTHER INFORMATION: 1
NAME/KEY: allele
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OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 2934
OTHER INFORMATION: 1
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NAME/KEY: allele
LOCATION: 6183
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NAME/KEY: allele
LOCATION: 6141
OTHER INFORMATION: NAME/KEY: allele LOCATION: 6338
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NAME/KEY: allele
LOCATION: 4109
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NAME/KEY: allele
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NAME/KEY: allele
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OTHER INFORMATION:
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NAME/KEY: allele
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NAME/KEY: allele
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LOCATION: 17555..2067
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LOCATION: 4062
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LOCATION: 2623
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INFORMATION: exon
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Best Local Similarity
Matches 207; Conserv
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LOCATION: 8926
OTHER INFORMATION: 1
NAME/KEY: allele
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LOCATION: 6375
OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: allele
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: allele
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 6467
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OTHER INFORMATION:
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OTHER INFORMATION: 10-507-170
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 8658
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OTHER INFORMATION:
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LOCATION: 6484
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LOCATION: 13524
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LOCATION: 12429
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LOCATION: 8703
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<u>AATTAAACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAAATTGAA</u>
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11336

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11454

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RESULT 7
US-09-134-001C-150/c
US-09-134-001C-150/c
; Sequence 150, Application US/09134001C
; Patent No. 6380370
; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-150
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PRICIATION NUMBER: US 60/064,964
PRIOR PRICIATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 150
LENGTH: 927
TYPE: NUMBER
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  306 TACATTATGTTCTGCTTCATGTAAAATTGTGAATATTCTCTTAA 263
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                                                                                                                  ATTGATTAATGACATGAAGTGCACAACACTAATTACTGGCCAGCTGTTGGCATTGTGTTT
                                                                                                                                                           TAATTTTTCATTAAAGATATTTGTGCAAATAAGATCTTTATCGTTAATATTCCCAGATAT
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49.7%;
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/OCCKET NUMBER: 9F/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEPAN: 503-5541-8589
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INFORMATION FOR SEQ ID NO:
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ORIGINAL SOURCE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 837 base pairs
TYPE: nucleic acid
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TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
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nes 212; Conserv
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    245
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TTAATGATGGTGTTTTATGACTAATACACTGATTTTTCAAGAAGGAAACCCATGTTAAAA 304
                                      TCTCACTGAATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAATGC 124
                                                                                                                                                                                                                                                                       TGAAATGAGATTATAATTTGAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATTATNC 244
                                                                                                                TAATTCTTATAAAAAGATTAAATAATAATAAATCAACATAATATTTATAAAAAATAGATATT 400
                                                                                                                                                    AGATAATTAAACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAAAT 184
                                                                                                                                                                                                                                                                                                             AGAAAAAGTTATTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCTATA 64
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Steiner, Sabine
Mohr, Christine
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Knechtle, Philipp
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                                                                                                                                                                                                                                                                                                                                                  Score 55.2; DB 3;
pred. No. 0.0072;
0; Mismatches 241;
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US-08-487-826B-13
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                                                                                      Matches
                                                                                                                                                                                                                                                              TELEPHONE: (619) 235-85;
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  NAME: IBraelsen, Ned REGISTRATION NUMBER: 29,655 REGISTRATION NUMBER: NITTELECOMMUNICATION INFORMATION: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/487,826B FILING DATE: 10-SEP-1993 CLASSIFICATION: 435
                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Israelsen. Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                               LENGTH:
                              223
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                                                                                   cch 7.4%; Score 53; DB 2; Length 19124; al Similarity 45.7%; Pred. No. 0.026; 215; Conservative 0; Mismatches 253; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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T: 620 Newport Center Drive 16th Floor
Newport Beach
California
                                                                                                                                                                                                                               nucleic acid
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                                                  GAAAAAGTTATTTTAATTTTCTATTAAACATTCTCTCAAAGCATTATTTTTATCCTATAT
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Miller, Louis H.
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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US-08-998-416-186
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TELEPAX: 919-541 INFORMATION FOR SEQ ID NO: 1/ SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: Sequence 186, Application US/08998416 Patent No. 6239264 GENERAL INFORMATION: APPLICANT: APPLICANT:
APPLICANT:
APPLICANT: APPLICATION NUMBER: US/08/998, FILING DATE: 24-DEC-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: CH 0016/97 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy APPLICANT: TELECOMMUNICATION INFORMATION: CORRESPONDENCE ADDRESS: APPLICANT: NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS COUNTRY: ADDRESSEE: 27709 T: 3054 Cornwallis Road Research Triangle Park : No. 6239264th Carolina Rebischung, Corinne
VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
VENTION: AND USES THEREOF
EQUENCES: 1152 USA Pohlmann, Rainer Steiner, Sabine Wendland, Jurgen Knechtle, Philipp Monr, Philippsen, 919-541-8587 No. 6239264artis Corporation Christine Rainer US/08/998,416 Peter Version #1.30

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RESULT 11
US-08-487-826B-13/c
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GOFTWARE: PATELLATA
GOFTWARE: PATELLATION DATA:
CURRENT APPLICATION NUMBER: US/08
APPLICATION NUMBER: US/08
APPLICATION 10-SEP-1993
                                                                                                                                                                                                                                                                                       APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
                                                                                                                                                   COUNTRY:
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TOPOLOGY: linear
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                                                                                                                                                                    Newport Beach : California
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620 Newport Center Drive 16th
                                                                                                                                                                                                                                                                                                           Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
                                                    PatentIn Release #1.0, Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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HYPOTHETICAL:
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REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
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ATTORNEY/AGENT INFORMATION:
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Local Similarity 45.8%;
18023 TAAATAAATAAAT 18011
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                                                                                              TTTTATTTTAAAAAATAAGCCTGTGTTCAAGCTCTGATCATATTTCTTTTTATTTTTGATTTT 368
                                                                GGAANAAAATACT
                                                                                                                              TGAGATTATATTTTTTTTTTCGCTCGGATTATTCAGAATTAGAGTAACAAAAAATAAAAC 1808
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                                                                                                                                                             TGATGGTGTTTTATGACTAATACACTGATTTTTCAAGAAGGAAACCCATGTTAAAAATAT 308
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Pred. No. 0.065;
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US-07-991-867B-23
US-07-991-867B-23
; Sequence 23, Application US/07991867B
; Patent No. 5476781
; GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
IP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Tloppy disk
COMPUTER SYSTEM: PC-DOS/MS-DOS
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RESULT 13
US-08-107-755A-23
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                                                                                                                                                                                     Sequence 23, Application US/08107755A
Patent No. 5721352
GENERAL INFORMATION:
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                   APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Hall, Richard E.
APPLICANT: Griddl, Michael E.
TITLE OF INVENTION: No. 5721352el Er
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSE: DAVID R. Saliwanchik
STREET: 2421 N.W. 41st Street, Su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 678 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: unk:
MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
PILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: WO 92/14818
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APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
        STREET:
CITY: C
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          Gainesville
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E: DNA (genomic)
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46.1%;
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                            Suite
                                                                                                            Entomopoxvirus
                                                                                                          Expression System
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                                                                                                                                              RESULT 14
US-08-544-332-23
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                                                                                                   sequence 23, Application US/08544332
Patent No. 5935777
GENERAL INFORMATION:
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COUNTRY: U.S.A.
ZIP: 32606
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
ODERATING SYSTEM: PC-DOS/MS-DOS
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (904) 372-580 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/82:
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/65:
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/827,658
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REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,755A
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TYPE: nucleic acid
STRANDEDNESS: double
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Local Similarity 46.1%;
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                                                                                                                                                                                                                                                                                                                                                                       TTAATGATGGTGTTTTATGACTAATACACTGATTTTTCAAGAAGGAAACCCATGTTAAAA
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: UF1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Gerard
STREET: 2421 N.W.
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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EDNESS: double
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2421 N.W. 41st Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   904-372-5800
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IBM PC compatible
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Pred. No. 0.069;
0; Mismatches 194;
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US-09-370-861A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: NO. 6410221el Entomopoxvirus
FILE REFERENCE: UP114.C4.D1
CURRENT APPLICATION NUMBER: US/09/370,861A
CURRENT FILING DATE: 1999-08-09
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PRIOR FILING DATE: 1991-02-19
NUMBER OF SEQ ID NOS: 78
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PRIOR FILING DATE: 1993-08-19
PRIOR APPLICATION NUMBER: WO 92/14818
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SUMMARIES

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Cancer-associated nucleic acids and polypeptides Patent: JP 2001516009-A 495 25-SEP-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH
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PD 25-SEP-2001
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PR 17-UUL-1997 US 08/996164,10-OCT-1997 US 60/061599
10-OCT-1997 US 60/061765,10-OCT-1997 US 08/948705 PR
11-OCT-1997 GB 9721697.2,22-UUN-1998 US 09/102322 PI
JOLD, MATTHEW J SCANLAN, ELISABETH STOCKERT, ALI GURE, YAO PI
                                                                                                                                                                                                                                           AAATACTGTTTCTGATAGCATGAAAATTTTTTAGATTTTTAATCTCNCTAATTTT
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NGAATAACCTTAAATATACTTTGTTAGCCAAACAAAACTTTTTTGTTTACATAGTTCTTT
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OZLEM TURECI,
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/mol_type="genomic DNA"
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98 c 85 g 25
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Location/Qualifiers
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Pred. No. 1.4e-91;
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(SCP-X/SCP-2) gene, ex
U11313
U11313.1 GI:532077
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Submitted (24-JUN-1994) Jerome F. Strauss III, Department of Submitted (24-JUN-1994) Jerome F. Strauss III, Department of Obstetrice and Gynecology, Division of Reproductive Biology, University of Pennsylvania Medical Center, 778 Clinical Research Building, 422 Curie Boulevard, Philadelphia, PA 19104-6142, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1052)

Ohba, T., Rennert, H., Pfeifer, S.M., He, Z., Yamamoto, R., Holt, J.A.,

Billheimer, J.T. and Strauss, J.F. III.

The structure of the human sterol carrier protein 2 gene (SCP2)

Genomics 24 (2), 370-374 (1994)

95213031
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                  /gene="SCP-X/SCP-2"
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protein-2"
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U11304.1:26...89,U11305.1:26...12,U11304.1:26...176,
U11307.1:26...173,U11308.1:26...133,U11309.1:1547...1700
U11310.1:26...128,U11311.1:26...155,U11312.1:26...105,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="1"
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                                    CATA-TTAACTTTGTAATGCACAGTTGT
                                                         CCTATTTAACTTTGTTATGCACAGTTGT
                                                                                                                                 TTGGATTTTACTGTTCCTAATTTTATTCTGAAACTCCATTTTTTCCCCCAGACCATAATTAC
                                                                                                                                                                           AGAATAATCCTTAAATATACTTTGTAAGCAAAACAAAAGCTTT
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Pred. No. 4.6e-85;
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OMFGYAGKEHMEKYGTKIEHFAKIGWKNHKHSVNNPYSGPODEYSIDEVVAASKEVPDP
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DIGGAVVVTLYKMGFPEAASSFRTHQIEAVGKSGVLPNSDKKADCTITMADSDFLALM
TGKMNPQSAFFQGKLKITGNMGLAMKLQNLQLOPGNAKL"

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    not
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KEYWORDS
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ORGANISM
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HUMSCP2A/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               He,Z., Yamamoto,R., Furth,E.E., Schantz,L.J., Naylor,S.L., George,H., Billheimer,J.T. and Strauss,J.F. III.
GEDNAs encoding members of a family of proteins related to human sterol carrier protein 2 and assignment of the gene to human chromosome 1 p21---pter protein 2 and assignment of the gene to human chromosome 1 p21---pter protein 2 and assignment of the gene to human chromosome 1 p21---pter protein 2 and assignment of the gene to human chromosome 1 p21---pter page 2 and 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Dec 6, 1993 this sequence version replaced gi:410029. Original source text: Human liver cDNA to mRNA.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sterol carrier protein-2,
Homo sapiens (human)
Homo sapiens
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/gene="SCP-X/SCP-2"
/evidence=experimental
2572
                                                                                                                                                                                                                                                                                                                    /gene="SCP-X/SCP-2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  MARQLIQGGVAECVLALGFEKNSKGSLGIKFSDRTIPTDKHVULLINKYGLSAHPVAF
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1932. .1937
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22. .1665
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2341. .2346
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                                                                                                     /gene="SCP-X/SCP-2"
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="sterol carrier
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Mclay, K.
Direct S
                                                                                                                                                        AL358233.3 GI:9797852
HTG; HTGS_PHASE1; HTGS_CANCELLED
Homo sapiens (human)
                                                                                                                                                                                                                                                             AL358233 122176 bp DNA
Homo sapiens chromosome 1 clone RP5-835A17,
PROGRESS ***, 8 unordered pieces.
                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                Homo sapiens
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/evidence=experimental
439 c 570 g
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98.1%;
                                                                               Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.5e-85;
""ematches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1872
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misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LU8752; 100% of reads
Sequencing vector: plasmid; LU8752; 100% of reads Chemistry:
Dye-terminator ET-amersham; 20% of reads Chemistry
Dye-terminator Big Dye; 79% of reads
Consensus quality: 118880 bases at least Q40
Consensus quality: 120216 bases at least Q20
Consensus quality: 120279 bases at least Q20
Insert size: 121476; sum-of-contigs
Insert size: 136681; 7.7% error; agarose-fp
Ouality coverage: 4.05x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requestes: clonerequest@sanger.ac.uk
On Aug 12, 2000 this sequence version replaced gi:9214208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: dJ835A17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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30894
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37023
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/chromosome="1"
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84492. .117843
                                                                                                             /note="assembly_fragment:00580
fragment_chain:2"
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fragment_chain:1"
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fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                        /note="assembly_fragment:00948
fragment_chain:2"
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| ragment_chain:1"
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45481: gap of 100 bp
56788: contig of 11307 bp in length
56888: gap of 100 bp
84391: contig of 27503 bp in length
84491: gap of 100 bp
117843: contig of 33352 bp in length
117943: gap of 100 bp
122176: contig of 4233 bp in length.
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lone_lib="RPCI-5"
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13586: gap of 100 bp
10893: contig of 17307 bp in length
30993: gap of 100 bp
37022: contig of 6029 bp in length
37122: gap of 100 bp
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                                                                                  AC022728
AC022728.4 GI:7249198
HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 175046)
                                                                                                                                                                      AC022728 175046 bp Homo sapiens chromosome 1 clone SEQUENCE, 34 unordered pieces.
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31142 a 30481 c 29651 g 30201 t
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117944. .122176
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98.1%;
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 Nusbaum, C.
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Pred. No. 1e-85;
D; Mismatches
                                                                                                                                                                                                                                                                                                                                            686
                                                                                                                                                                                          DNA linear
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     and Lander, E.
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All repeats were identified mains constitution.
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Submitted (06-FEB-2000) Whitehead Institute/MIT Center Submitted (16-FEB-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 175046)
                                                        Center project name: L5491

Center clone name: 310 J 14

Center clone name: 310 J 14

Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 156135 bases at least Q40

Consensus quality: 166373 bases at least Q30

Consensus quality: 168380 bases at least Q20

Insert size: 185000; agarose-fp

Ouality coverage: 3.4 in Q20 bases; agarose-fp

Quality coverage: 3.6 in Q20 bases; sum-of-contigs
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NOTE: This is a 'working draft' sequence. It currently
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
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consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                 source
                                                                                                                                                                                                                                                                               corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (04-APR 2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 7, 2002 this sequence version replaced gi:17939714. During sequence assembly data is compared from overlapping clones. Where differences are found these are anotated as variations cogether with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                RP11-334A14 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Human DNA sequence from clone RPI1-334A14 on chromosome
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                                                                                                                       //www.chori.org/bacpac/home.htm
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                    Location/Qualifiers
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RESULT 8
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           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1439)
                                                                                                    IMAGE:4287946, mRNA,
BC005911
                                                                                                                           Homo sapiens,
Ştrausberg, R.
                                                   Homo
                                                                                        BC005911.1 GI:13543502
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/clone="RP11-334A14"
/clone_lib="RPCI-11.2"
/ 45351 c 44031 g 53577
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissus Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Gen
Center, Stanford University School of Medicine, Stanford, CA
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                         TTTAAAAATATAGCCTGTGTTCAAGCTCTGATCATATTTCTTTTATTTTTGATTTGGGAAGA 360
                                                                                                                      TGTTTTATGACTAATACACTGATTTTTCAATAAGGAAACCCCATGTTAAAAATATTTTTAT
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TTTAAAAATAAGCCTGTGTTCAAGCTCTGATCATATTTCTTTTATTTTGATTTGGGAAGA
                                                                                            TGTTTTATGACTAATACACTGATTTTTCAATAAGGAAACCCCATGTTAAAAAATATTTTTAT
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EQFVKKIGGIFAFKVKDGFGGKEATWVDVKNGKGSVLPNSDKKADCTITMADSDFLA
LMTCKNNPOSAFFQCKLKITGNMGLAMKLQNLQLQPGNAKL"
219 c 272 g 458 t
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/protein id="AAH05911.1"
/db_xref="GI:13543503"
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/tissue_type="Brain, primitive ne
/clone_lib="WIH_MGC_56"
/lab_host="DH10B"
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/db_xref="LocusID:6342"
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PP 15-JUL-1998 JP 2000503425

PR 17-JUL-1997 US 08/986164,10-OCT-1997 US 08/948705 PR 10-OCT-1997 US 08/948705 PR 11-OCT-1997 US 09/102322 PI 11-OCT-1997 GB 9721697.2,22-JUN-1998 US 09/102322 PI 11-OCT-1997 US 09/102322 PI 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 714)

Old, L.J., Scanlan, M.J., Stockert, E., Gure, A., Chen, Y.T., Gout, I., Ochare, M., Obata, Y., Pfreundschuh, M., Tureci, O. and Sahin, U. Cancer-associated nucleic acids and polypeptides
Patent: JP 2001516009-A 494 25-SEP-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH
                                                                                                                                                                                                                                        A61P35/00,
PC C07K14
PC C12N15
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I UGUR SAHIN
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JP 2001516009-A/494
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                                                      /organism="Homo sapiens"
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/db_xref="taxon:9606"
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 GenBank staff at the National Library of Medicine created entry [NCBI gibbsq 122504] from the original journal artic This sequence comes from Fig. 1.
                                                                  Localization of human sterol expression in COS-7 cell Hokkaido Igaku Zasshi 67 (6), 93131254
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sapiens
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Primates;
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2 (human,
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                                                                                839-848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494;
sterol carrier protein-2.
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae;
                                                                             M55421
M55421.1 GI:432978
                                                                                                            Human sterol
                                                                                                                           HUMSTEAA
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                                                                                                                                                                                                                     CCTATTTAACTTTGTTATGCACAGTTGT
                                                                                                                                                                                                                                                                              TTGGATTTTACTGTTCCTAATTTTATTCTGAAACTCCATTTTTCCCCAGACCATAATTAC
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EQFVKKIGGIFAFKVKDGPGGKEDTWVVDVKNGQGSVLPNSDKKADCTITMAASDFLA
LMTGKMNPQSAFFQGPLKITGNMGLAMKLQNLQLQPGNAKL"
1 200 c 255 g 365 t
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/product="sterol carrier
/protein_id="AAB24921.1"
/db_xref="GI:263551"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens'
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="This sequence
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                                                                                                            carrier
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97.2%;
                                                                                                         1219 bp
: protein-2 (
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Pred. No. 3.7e-58;
0; Mismatches 11;
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VERSION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein 2
Proc. Natl. Acad. Sci. U.S.A. 88
91110550
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Yamamoto,R., Kallen,C.B., Babalola,G.O., Rennert,H.,
Billheimer,J.T. and Strauss,J.F. III.
Cloning and expression of a cDNA encoding human sterol
protein 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Dec 6, 1993 this sequence version replaced Original source text: Human female liver. Location/Qualifiers
                                                                             GACTAATACACTGATTTTTCAATAAGGAAACCCATGTTAAAAATATTTTTTATTTTAAAAA
                                                                                                                                    TGAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATTATTCTTAATGATGGTGTTTTAT 248
                    TAAGCCTGTGTTCAAGCTCTGATCATATTTCTTTTATTTTGATTTTGGAAAAAAATACTG
                                                            TGAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATTATTCTTAATGATGGTGTTTTAT
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                                                                                                                                                                                                                                                        402
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                /gene="SCP-2"
/evidence=not_experimental
1190. .1195
/gene="SCP-2"
/evidence=experimental
1219
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eqfvkkiggifafkvkdgpggkeatwvvdvkngkgsvlpnsdkkadctitmadsdfla
lmtgknnpgsaffqgklkitgnmglamklqnlqlqpgnakl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                 /gene="SCP-2"
/evidence=experimental
195 c 255 g
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/product="unnamed"
782. .787
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/evidence=not_experimental
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144. .512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="sterol carrier protein-2"
/protein_id="AAA03559.1"
/db_xref="GI:432973"
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SCP-2"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="SCP-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue type="liver"
|. .1219
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97.6%;
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                                                                                                                                                                              Score 440.4; DB 9;
Pred. No. 6.5e-56;
0; Mismatches 8;
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                                                                                                                                                                                 Indels
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TTTAAAAATAAGCCTGTGTTCAAGCCTCTGATCATATTTCTTTTATTTTGATTTTGGGAAGA
                                               NNTTTNANNACTAATNCCCNGATTTTCCAATANGGAANCCCNNNTTAAAANTNTTTTNAT
                                                                                                                                                                 CCTTNCTTGAAAANGGAAATTINTACCAANGGACNGAAANCNTINTAATTNGAANTNAAA
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Pred. No. 1.2e-51;
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CC Cancer-associated nucleic acids and polypeptides. FH Key
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PI IVAN GOUT, MICHAEL O'HARE, YUICHI OBATA, MICHAEL PFREUNDSCHUH, PI
OZLEM TURECI,
                                                                                                                                                                                                                                                                          PF 15-JUL-1998 JF 2000503425
PR 17-JUL-1997 US 08/896164,10-OCT-1997 US 60/061599
10-OCT-1997 US 60/061765,10-OCT-1997 US 08/948705 PR
11-OCT-1997 GB 9721697.2,22-JUN-1998 US 09/102322 PI
J OLD MATTHEW J SCANLAN,ELISABETH STOCKERT,ALI GURE,YAO PI
                                                                                                                                                                                                                                                                                                                                Old,L.J., Scanlan,M.J., Stockert,E., Gure,A., Chen,Y.T., Gout,I.,
OGhare,M., Obata,Y., Pfreundschuh,M., Tureci,O. and Sahin,U.
Cancer-associated nucleic acids and polypeptides
Patent: JP 2001516009-A 497 25-SEP-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH
OS Homo sapiens (human)
PN JP 2001516009-A/497
PD 25-SEP-2001
PF 15-JUL-1998 JP 2000503425
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Homo sapiens
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(bases 1 to 843)
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                                                                                        /organism='Homo
                        /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
184 c 89 g 21
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M75884.1 GI:432976
sterol carrier protein-2.
Homo sapiens (human)
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            DNA Cell Biol.
92029618
                                                                                                                                           Homo sapiens
                                                                                                                                                                                                            Human sterol carrier
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                                                                                                                                                                                                                                                                                                         CCTATTTAACTTTGTTATGCACAGTTGTT
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protein
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He,Z., Yamamoto,R., Furth,B.E., Schantz,L.J., Naylor,S.L., George,H., Billheimer,J.T. and Strauss,J.F. III. cDNAs encoding members of a family of proteins related to human sterol carrier protein 2 and assignment of the gene to human chromosome 1 p21---pter
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATTTTAATTTTCTTATAAACATTCTTCTCAAAAGCATTATTTTATCCTATATCTCACTGAA
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Pred. No. 1.2e-51;
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559-569 (1991)
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Original source text: Human liver cDNA to mRNA.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vesa,J., Hellsten,E., Branoski,B.L., Emanuel,B.S., Billheimer,J.T., Mead,S., Cowell,J.K., Strauss,J.F.III. and Peltonen,L. Messignment of sterol carrier protein X/sterol carrier protein 2 to 1p32 and exclusion as the causative gene for infantile neuronal cesoid lipofusionosis
                     CCCAGACCATAATTACCCTATTTAACTTTGTTATGCACAGTTGT 686
                                                                                                TTGTTTACATAGTTCTTTGGATTTTACTGTTCCTAATTTTATTCTGAAACTCCATTTTTC 642
                                                                                                                                               AAACTGAATCTTCAGCAGAATAATCCTTAAATATATTTTGTAAGCAAAACAAAAGCTTTT
                                                                                                                                                                    AAACTGAATCTTCAGCNGAATAA-CCTTAAATATACTTTGTTAGCCAAACAAAA-CTTTT 582
                                                                                                                                                                                                                     TAATTACTGGCCAGCTGTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGAAAACTCTT 1321
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CCCAGACCATAATTACCATA-TTAACTTTGTAATGCACAGTTGT 1158
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1218. 1223

19enem SCP-2"

/genem SCP-2"

/note="no polyA or polyA signal was found at the end of this cDNA clone, indicating that the mRNA sequence may be partial at the 3' end"

/evidence=not experimental
a 254 c 342 g 422 t
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82. .951
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1686	AI76168	9	ð	4	82.	37
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3310	AI68331	9	J	8	0	25
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0927	BQ00927	12	S		30.	15
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2415	CA4241	14	w	Ņ	w	13
6874	BM96874	12	N		63	12
287	A182628	9	J	Ņ	34.	11
2714	BU6271	13	S.		35	10
8537	BM98537	12	ū		35	9
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BQ014192
LOCUS
LOCUS
UI-H-ED1-axs-g-24-0-UI.sl NCI_CGAP_ED1 Homo sapiens cDNA clone
IMAGE:5833007 3', mRNA sequence.

ACCESSION
BQ014192
VERSION
EST.
SOURCE
Homo sapiens (human)
BQ014192.1 GI:19739093
EXTYWORDS
SOURCE
CORGANISM
Homo sapiens (human)
EURARYOCIS; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
NGI.CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NGI.CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
VIURNAL
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs -@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
COMMENT
Conse Distribution: Clone distribution information can be found
Chrough the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 317-343, >AT_rich#Low_complexity (matched compliment)

Result

Score

Query Match Length

DB

ä

Description

SUMMARIES

639 638.4 637.6 636.8

93.0 92.9 92.8 92.7

769 761 837 738

12 12 12

BQ014192 BM997078 AI566109 BQ045161

BQ014192 UI-H-ED1-BM997078 UI-H-ED0-AI566109 tn53e08.x BQ045161 UI-CF-EN1

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                                                          GTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGAAAACTCTTAAACTGAATCTTCAGC
                                                                                              GTTGGCATTGTGTTTCTTAGTTTCTCCCCAAGGAAAACTCTTAAACTGAATCTTCAGC
                                                                                                                                                                                       AAGAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACTAATTACTGGCCAGCT
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//dev_stage="Adult"
//dev_stage="Adult"
//lab_host="Delion (Life Technologies)"
/lab_host="PubloB (Life Technologies)"
//clone_lib="NCI_CGAP_ED1"
//note="Forgan: Left Publc Bone; Vector: pT7T3-Pac
//note="Forgan: Left Publc Bone; Vector: Delional Library Was constructed according to Bonaldo
//note="Forgan: Left Publc Bone; Vector: Delional Bone; Left Bone; Vector: Left Bonaldo
//note="Forgan: Left Bone; Vector: Left Bone; Vecto
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TAG_LIB=UI-H-ED1
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BASE COUNT
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TITLE
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.B. Consortium/LLML at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 761)
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UI-H-ED0-axo-f-03-0-UI.s1 NCI_CGAP_ED0 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Following repetitive elements were found in this CDNA sequence: 316-342, >AT_rich#Low_complexity (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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                                                                                                 library is GCTCAAGGCT.
TAG LIB-UI-H-EDO
TAG_TISSUE=chondrosarcoma
TAG_SEG=CGTCAAGGCT"
a 108 c 98 g 285 t
                                                                                                                                                                                                                       library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_ED0"
/clone_lib="NCI_CGAP_ED0"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
/paarmacia) with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCI_CGAP_ED0 is a cDNA library containing
the following tissue(s): Chondrossarcoma call line CS5. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5831426"
/tissue_type="Chondrosarcoma"
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92.9%;
98.1%;
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Score 638.4; DB 12;
Pred. No. 4.4e-66;
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Sequencing Center information can be

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AI566109
AI566109.1 GI:4524561
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Unpublished Contact: Robert Strausberg, Ph.D. Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 837)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                              Homo sapiens (human)
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Cente
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 619 Std Error: 0.00
Seq primer: -40UP from Gibco
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NGAATAA-CCTTAAATATACTTTGTTAGCCAAACAAACTTTTTTTGTTTACATAGTTCTT
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//note="Organ: kIdney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; plasmid DNA from the normalIzed library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2172134"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 6 (9),
97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (www.openbiosystems.com).

(The following repetitive elements were found in this cDNA sequence: 316-342, >AT rich#Low_complexity (matched compliment) seq.primer: M13 FORWARD
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2024 University of Iowa
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BQ045161.1 GI:19796248
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                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The
                                                                                                                                                                                                                         /dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (Tl phage resistant)
/clone lib="UI-CF-ENI"
/clone lib="UI-CF-ENI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-ENI is a normalized CDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to the containing t
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/tissue_type="Primary Lung Cystic Fibrosis Epithelial
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/mol_type="mRNA"
/db_xref="taxon:9606"
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.F., Lennon,G. and Soares,M.B.
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BU619082
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 712)
                                                                            Homo sapiens
                                                                                                                                                             BU619082.1
                                                                                                    Homo sapiens (human)
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Email: cgapbs r@mail.nih.gov

Tissue Procurement: James Martin

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@ulowa.edu

The following repetitive elements were found in this cDNA sequence: 1-32, AT richHlow_complexity (matched compliment) 298-324, AT richHlow_complexity (matched compliment)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/ Clone | Ibs=WCI COAP FHI |
/ Notes=Torgan: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia |
/ Notes=Torgan: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia |
/ Notes=Torgan: Chondrosarcoma; Vector: pT7T3-Pac |
/ Notes=Torgan: Chondrosarcoma 
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/tissue_type="Cell Line"
/dev_stage="Adult"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

The following repetitive elements were found in this cDNA

sequence: 319-345, >AT rich#Low_complexity (matched compliment)

Seg primer: M13 FORWARD
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BQ008197.1 GI:19733097
EST.
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1 (bases 1 to 751)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone_lib="NCI_CGAP_ED1"
/clone="Organ: Left Pubic Bone; Vector: pT7T3-Pac
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCI_CGAP_ED1 is a normalized CDNA library
containing the following tissue(s): Chondrosarcoma cell
                                                                                                                             /tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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TAG_SEQ=CGTCAAGGCT"
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Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 316-342, >AT_rich#Low_complexity (matched compliment)
Seq_primer: M13 FORWARD
POLYA=Yes.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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BU619112
BU619112.1 GI:23285327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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ACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAAATTGAAATGAGA 180
                                                                                                                           TTTTAANAAATAACATTAGTATTAGAAAAAACTAGGAAAAAAAGATNAATGCAGATAATTAA 120
                                                                                                                                                                             ATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCTATATCTCACTGAA
                                                                       TTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAGATAAATGCAGATAATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                    269
                                                                                                                                                                                                                                                                                   Conservative
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//dev stage="Adult"
//lab_nost="DH10B (Life Technologies)"
//clone_lib="NCI_CGAP_FH1"
//note="Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia / note="Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia / with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FH1 is a normalized cDNA hibrary betained from a cell_line_derived from grade I chondrosarcoma tissue.
The library was constructed and normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of coligonucleotide used to prime the synthesis of that is
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was provided
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="UI-H-FH1-bfm-1-10-0-UI"
/tissue_type="Cell Line"
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_xref="taxon:9606"
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97.8%;
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Pred. No. 8.8e-66;
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                                                                                                                                                                                                                                                                                                                                                                         wc66,04.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2314423 3' similar to gb:552450 NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (HUMAN); mRNA sequence.
                                                 Email: Cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1429 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 439.
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 714)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                            Unpublished
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/organism="Homo sapiens"
/mol_type="mRNA"
                                         Location/Qualifiers
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CTATTTAACTTTGTTATGCACAGT 683
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/lab_host="DH10B"
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/clone="IMAGE:2314423"
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Pred. No. 1e-65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares
DNA Sequencing by: Dr. M. Bento Soares
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The following repetitive elements were found in this cDNA sequence: 316-342, -AT_rich#Low_complexity (matched complir Seq primer: M13 FORWARD
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two appr
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (www.openbiosystems.com).
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                                                                                                                                                                                                                                                                                                               /note=\(\text{Torgan}: \) Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-GP-ECI is a normalized CDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA as ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime sequence that is located between the Not I site and the Actrocture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                   _TISSUE=Normal Lung
                                                                                                                                                                                                                                                                               LIB=UI-CF-EC1
                                                                                               92.5%;
                                                                                                                                                                                         SEQ=AAGTGCTTAC"
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                                                                                            Score 635.2; DB Pred. No. 1e-65;
                                                                          Mismatches
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BU627147.1
EST.
                         Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Martin

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained
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                                                                                                                                                         Tumor Gene Index
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762 bp mRNA linear EST 23-SEP-20 UI-H-FG0-bct-i-12-0-UI.sl NCI_CGAP_EN1_2 Homo sapiens cDNA clone UI-H-FG0-bct-i-12-0-UI 3', mRNA sequence.
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                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 762)
                                                                                                                                                                                                                                                                                    Homo sapiens
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in
                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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309-335, >AT rich#Low complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA-Yes.
GTTGGCATTGTGTTTCTTACTTACTTCTCCCAAGGAAAACTCTTAAACTGAATCTTCAGC
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/tissue_types "Enchondroma cell line"
/dev_stages "Adult"
/lab host="DHIOB (Life Technologies)"
/clone_lib="NCI_CGAP_ENI_2"
/clone_lib="NCI_I lines"
/clone_lib="NCI_CGAP_ENI_2"
/clone_lib="NCI_I lines"
/clon
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TAG_TISSUE=Enchondroma cell line (Mix of EN1
TAG_TISSUE=EncGTCACTC"
TAG_SEQ=CGGTCACTC"
109 c 97 g 286 t 1 others
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                                                                               671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1454 Std Error: 0.00

Seq primer: -40UP from Gibco
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 770)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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ilarity 97.5%;
Conservative
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Location/Qualifiers
                                                                                                                                                                                   /tissue_type="normal prostate"
//lab host="phioB"
//clone_type="NCI_GAP_pr22"
//clone_lib="NCI_GAP_pr22"
//note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
//note="Organ: prostate; Vector: pt7T3D-Pac (Pharmacia)
//note="Organ: prostate bulk tissue, and was then primed with
a modified polylinker; lst strandcdcDNA was
a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
71 a lll c 99 g 285 t 4 others
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/db_xref="taxon:9606"
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           University of Iowa
2024 University of Iowa
Tel: 319 356 4866
Fax: 319 356 7171
                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 721)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to fac
                                                                                                                                                                                                                                                                         BM968746 721 bp mRNA linear UI-CF-DU1-aam-a-03-0-UI.51 UI-CF-DU1 Homo sapiens UI-CF-DU1-aam-a-03-0-UI 3', mRNA sequence.

EM968746 BM968746 GI:19586333 EST.
                                                                                                                                                                                                                                            Homo sapiens
Email: paul-mccray@uiowa.edu
                                                                          McCray Lab
                                                                                      Contact: McCray,
                                                                                                        8889548
                                                                                                                                  Genome Res. 6 (9), 791-806 (1996)
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               AAATACTGTTTCTGATAGCATGAAATGCAAAATTTTTAGATTTTTAATCTCACTAATTTT
                                                                                           TTTAAAAATAAGCCTGTGTTCAAGCTCTGATCATATTTCTTTTATTTTTGATTTTGGGAAGA
                                                                                                                                      TGTTTTATGACTAATACACTGATTTTCAATAAGGAAACCCATGTTAAAAATATTTTTAT
                                                                                                                                                       TGTTTTATGACTAATACACTGATTTTTCAATAAGGAAACCCATGTTAAAAATATTTTTAT
                                                                                                                                                                                                  TTATAATTTGAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATTATTCTTAATGATGG
                                                                                                                                                                                                                                                              <u>ACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAAATTGAAATGAGA</u>
                                                                                                                                                                                                                                                                             ACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAAATTGAAATGAGA
                                                                                                                                                                                                                                                                                                                        TTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAATGCAGATAATTAA
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420 390 360

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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The following repetitive elements were found in this sequence: 315-341, >AT rich#Low_complexity (matched comprimer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (www.openbiosystems.com).
ATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCTATATCTCACTGAA
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/lab_host="DH10B (Life Technologies)
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/db_xref="taxon:9606"
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                                                                                                                                                                                                92.0%;
                                                                                                                                                                                                Score 632; DB 12;
Pred. No. 2.5e-65;
                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                Length
                                                                                                                                                     Indels
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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-48, ART rich#Low complexity (matched compliment)
314-340, ART rich#Low complexity (matched compliment)
Seq primer: M13 FORWARD
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1 (bases 1 to 734)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                   POLYA-Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGAATAA-CCTTAAATATACTTTGTTAGCCAAACAAAA-CTTTTTTTGTTTACATAGTTCT
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/tissue type="Cell lines"
//dev stage="MADULT"
//lab_host=="MH10B (Life Technologies)"
/clone lib="NCI CGAP FEL"
/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia ) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FEL' |
I; NCI CGAP FEL' | sa normalized cDNA library derived from a pool of mENA obtained from 3 cell lines from grade II chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is
                                                                                                                                                                                                                                                                                              g
b
                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FE1-bdv-m-12-0-UI"
                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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                              wx25e05.xl NCI CGAP Kidll Homo sapiens cDNA clone IMAGE:2544704 3' similar to gb:S52450 NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (HUMAN), mRNA sequence.
AW052045.1 GI:5914404
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     sapiens (human)
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CATA-TTAACTTTGGTATGCACAGTTGT
                                                                            TTGGATTTTACTGTTCCTAATTTTATTCTGAAACTCAATTTTACCCCCAGACATAATTAC
                                                                                                   TTGGATTTTACTGTTCCTAATTTTATTCTGAAACTCCATTTTTCCCCCAGACCATAATTAC
                                                                                                                                                         AGAATAATCCTTAAATATACTTTGTAAGCAAAACAAAAGCTTTTTTGTTTACATAGTTCT
                                                                                                                                                                                                                                      GTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGAAAACTCTTAAACTGAATCTTCAGC
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ilarity 97.5%;
Conservative
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of Iowa.
TAG_LIB-UI-H-FE1
TAG_TISSUE=Human grade 2
TAG_SEQ=CGCTACGGAC"
TAG_SEQ=CGCTACGGAC"
27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  located between the Not I site and the (dT)18 tail. sequence tag for this library is CGCTACGGAC. The celines were provided by Dr James Martin from the Uni
                                                                                                                                                                                                                                                                                                                                                                                                  CTGATAGCATGAAATGCAAAATTTTTAGATTTTAATCTCACTAATTTT
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Pred. No. 2.5e-65;
0; Mismatches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Chri. Emmert-Buck, M.D., Ph.D.
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Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 786)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs remail.nih.gov

Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consorthum/LLML at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 316-342, ART_rich#Low_complexity (matched compliment)
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BQ009270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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/clone lib="NCI_GAP_ED1"
/clone lib="NCI_GAP_ED1"
/clone "Organ: Left Pubic Bone; Vector: pT7T3-Pac
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
/pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line CS5. The library was constructed according to Bonaldo
, Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
                                                                                                                                                                                                                                                                                                                                                         /dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="Chondrosarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="IMAGE:5835073"
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        CCTATTTAACTTTGTTATGCACAGTTGT 686
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                            TTGGATTTTACTGTTCCTAATTTTANTCTGAAACTCAATTTTTACCCCCAAGACCATATTA
                                       TTGGATTTTACTGTTCCTAATTTTATTCTGAAACTCCATTTTTCCCCAGACCATAATTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                    sequence tag for this library is GCTCAAGGCT.
TAG_LIBBUT-H-ED1
TAG_TISSUB-chondrosarcoma
TAG_SEO-CGTCAAGGCT"

105 c 96 g 281 t 2 others
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Search completed: November 27, 2003, 12:28:12 Job time: 1852.59 secs

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Database
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N_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Human immune

ALIGNMENTS

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(LUDW-) LUDWIG INST CANCER RES.			10-OCT-1997; 97US-0948705.	10-OCT-1997; 97US-0061765.	10-OCT-1997; 97US-0061599.				15-JUL-1998; 98WO-US14679.		28-JAN-1999.		WO9904265-A2.		Homo sapiens.			cancer; colon cancer; gastric o	Cancer associated antigen; diagnosis; research; treatment; human;		Gastric cancer associated gene.		02-JUL-1999 (first entry)		AAX40095;		ID AAX40095 standard; DNA; 687 BP.	RESULT 1

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
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diagnosis, monitoring
                     NGAATAACCTTAAATATACTTTGTTAGCCAAACAAAACTTTTTTGTTTACATAGTTCTTT
                                                                                    GTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGAAAACTCTTAAACTGAATCTTCAGC
                                                                                                                                                       AAGAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACTAATTACTGGCCAGCT
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Scanlan MJ,
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Pred. No. 4.6e-108;
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2639

ATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCTATATCTCACTGAA

Query Match

Local

Similarity

92.7%; 98.0%;

Score 636.8; | Pred. No. 3.4e

6.8; "" 5. 3.4e-100;
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Gaps

2580 60 674;

Conservative

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RESULT 2
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ID AAH57551
XX AAH575
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                                                             assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetries, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposicion to a disorder where the gene is associated with a
                                                                                                                                                                                                                                                                                                        AAH57161 to AAH57576 represent cell and tissue specific polynucleotide sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology -
    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
metabolic disease; developmental disease; cytostatic; immunomodulatory;
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                                             immunopathology or neuropathology.
      2663 BP; 807 A; 472 C;
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10-OCT-1997;
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10-OCT-1997;
11-OCT-1997;
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WPI; 1999-132448/11

New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers

Claim 67; Page 695; 787pp; English.

The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and cancer.

Sequence 714 BP; 258 A; 100 Ç 92 ဂ 260 T; 4 other;

Query Match Best Local Similarity

89.1%; 97.1%;

Score 611.8; DB 2 Pred. No. 6.5e-96;

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                                                                                                                                                                                                                                                 The invention relates to a human colon tumour expressed polynucleotide (I) encoding a polypeptide (II, ABB679991-ABB67996) comprising; (i) any of 2600 fully defined nucleotide sequences (ABW8669-ABW89289); (ii) complements of (i); (iii) at least 20 contiguous residues of (i); (iv) sequences that hybridize to (i), under moderately stringent conditions; (v) sequences having at least 75% or 90% identity to (i); or (vi) degenerate variants of (i). The compositions and methods of the present invention are useful for the diagnosis, prevention and/or treatment of cancer, particularly colon cancer. (I) can be used in gene therapy and (I) and (II) are useful in pharmaceutical compositions such as vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated tumor colon polynucleotide and polypeptide, useful for the diagnosis, prevention and/or treatment of cancer, in particular colon cancer -
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06-FBB-2001; 2001US-2670IP.
28-WAR-2001; 2001US-279670P.
10-JUL-2001; 2001US-304037P.
                                                                                                                                                                                                           Sequence 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 578; 266pp + Sequence Listing; English
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                                                                                                        Chen Y, Gout
Pfreundschuh
                                                                                                                                                                                                                                                                                                                                          Cancer
breast
                             New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
          Claim 67; Page 696;
                                                                          WPI; 1999-132448/11.
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Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ဂ္
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.8e-62;
701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T; 118 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
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                                                                                                673
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RESULT 6
AAT19975/c
ID AAT19975 standard; cDNA to mRNA;

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                                                                                                                                                                                                                                                                                                                                                               A single-stranded DNA (or its complementary strand or the corresp. Couble-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; swithesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-206931/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matsubara K, Okubo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reflects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUL-1996
                                                                                                                                                                                                                                                                                                                                                     recognising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                              180
 154
                                                             214
                                                                                                                           274
                                                                                                                                                                                         334
                                                                                                                                                                                                                                                         324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene signature
                                                                                                                                                         60
                                                                                                                                                                                                                                                                          Similarity
                  ATTATAATTTGAAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATTATTCTTAATGATG 239
                                                                                                                                                                                         ATTTTAATTTCCTATTAAACATNCTCCTCAAAGCATTATTTTANCCCTATATCTCACTGA
                                                                                                                                                                                                             ATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTAT-CCTATATCTCACTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page
                                                                              AACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAAATTGAAATTGAG
                                                                                                                           ATTTTAAGAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAATGCAGATAATTA
                                                                                                                                            ATTTTAANAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATNAATGCAGATAATTA 119
                                                                                                                                                                                                                                                                                                                        351 BP; 117
                                                             AACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAAATTGAAATGAG
                                                                                                                                                                                                                                                                                                                                                       different cell types.
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  525; 2245pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93JP-0355504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-JP01916
                                                                                                                                                                                                                                                                      43.8%;
97.0%;
                                                                                                                                                                                                                                                                                                                       A; 44 C; 44 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMGS01107
                                                                                                                                                                                                                                                         <u>,</u>
                                                                                                                                                                                                                                                                        Score 300.8; DB 16; Length Pred. No. 7.8e-43;
                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                       141 T;
                                                                                                                                                                                                                                                                                                                        5 other;
                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Each library abundance of
                                                                                                                                                                                                                                                                                         351;
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                                                                                                                              RESULT 7
AAH57293/c
ID AAH57293 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                               Query Match
Best Local S
Matches 261
                                                                                                                                                                     mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of [1] in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, prognosis or monitoring of treatments and for investigating a predisposis or monitoring of treatments and for investigating a predisposis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a
                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                     sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                                                    AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 117; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated with a cancer, immunopathology or neuropathology -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sornasse T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-NOV-2000; 2000WO-US30396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200132927-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lung; liver; uterus;
metabolic disease; de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human liver specific cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH57293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE GENOMICS INC
                                                  Local 261;
                               243 TTTTATGACTAATACACTGATTTTCAATAAGGAAACCCATGTTAAAAATATTTTTATTT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
                                                                              Similarity
                                                                                                                                                           immunopathology or neuropathology.
                                                                                                                              262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       er; uterus; ovary; stomach; intestine; kidney; pancreas; ss; disease; developmental disease; cytostatic; immunomodulatory; ective; gene therapy; cancer; immunopathology; neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTTTTAAAAATAAGCCTGTGTTCAAGCTCTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTTTAAAAATAAGCCTGTGTTCAAGCTCTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGTTTTATGACTAATACACTGATTTTTCAATAAGGAAACCCATGTTAAAAATATTT-TT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGTTTTATGACTAATACACTGATTTTTCAATAAGGAAACCCATGTTAAAAATATTTNTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seilhamer JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specific; diagnosis; brain; heart; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9905-0163508
                                                                                                                              103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA;
                                                                              38.0%;
                                                                                                                             A; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262
                                                                                                                             ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watson
                                                             Score 261; DB 22;
Pred. No. 4.8e-36;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                                                              3
4
                                                                                                                             G; 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO:133
                                                                                                                           T; 0 other;
                                                                                           22;
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                                                                                           Length 262;
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                             Gaps
203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35
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RESULT 8
ABX83093/c
ID ABX830
XX ABX830
XX ABX830
XX ABX830
XX ABX830
XX ABX830
XX Corn e
XX Corn e
XX Corn e
XX Corn e
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XX INSCAPA
XX INCY-
XX INSCAPA
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XX INSCAPA
XX INSCAPA
XX INSCAPA
XX INCY-
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XX INSCAP
                                                                                                                                                                                                                                          The present invention relates to the isolation of corn ear-derived polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMON022 and SATMON023. Some of the cpds uniquely identify structural, functional, and regulatory genes of corn ear. The polynucleotides sequences are useful for detecting cpds in a sample, for producing a corn ear-specific profile of gene transcription, for detecting altered gene expression in inbred or hybrid plants, and for screening several molecules for specific binding to the polynucleotide. The cdps are useful to identify, isolate or expression in the constraint of the polynucleotide.
are useful to identify, isolate, or extend identical or related corn-ear nucleic acid sequences from DNA libraries, and in nucleic acid amplification or hybridisation techniques to follow the expression of desirable traits through plant breeding programs. Preferably, the cdps are used to identify, evaluate, alter, or follow the inheritance of desired characteristics associated with growth and development, disease resistance, environmental adaptabil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SATMON023; structural gene; functional gene; regulatory gene; corn ear-specific profile; gene transcription; gene expression; hybrid plant; desirable trait expression; plant breeding program; inheritance; desired characteristic; growth; development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel purified corn-ear derived polynucleotide useful as hybridization probe for detecting polynucleotide in sample, and for identifying, evaluating, and altering desired characteristics associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Examples; SEQ ID No 1553; 390pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-208840/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        multigene trait;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corn ear-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE GENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease resistance; environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAACTATTGAGAAATTGAATTAATGACATGAAGTGCACAACACTAATTACTGGCCAGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATACTGTTTCTGATAGCATGAAATGCAAAATTTTTTAGATTTTTAATCTCNCTAATTTTAA 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGCATTGTGTTTCTTACTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sherman BK;
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       environmental adaptability
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Best Local S
Matches 161
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76489/c
AAQ76489
                                                                                                                                                                          Gross J,
Sibson D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality, and yield of corn. The cdps are also useful as molecular markers for studying inheritance and multigene traits in a plant breeding program. The cpds are useful for producing purified corn-ear polypeptides by recombinant techniques. They are also useful in diagnostic assays to detect or confirm conditions or diseases associated with abnormal levels of cdp expression. ABX81541-ABX89140 represent corn ear-derived polynucleotides (cpds) of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html.
                    Human nucleic acid fragments, isolated from brain adrenal tissue, the placenta or bone marrow comprise any of: (A) a sequence selected from (AAQ76401-Q77613), (B) an allelic variation of a sequence as described in (A), or (C) a sequence complementary to (A) or (B).
            to (A) or (Updated c
                                                                                         Claim 1; Page 64; 616pp;
                                                                                                               New nucleic for genetic
                                                                                                                                                                                                                                      13-JUL-1992;
                                                                                                                                                                                                                                                            13-JUL-1993;
                                                                                                                                                                                                                                                                                    20-JAN-1994.
                                                                                                                                                                                                                                                                                                          WO9401548-A2
                                                                                                                                                                                                                                                                                                                                                       Brain; placenta; bone marrow detection; homology; human;
                                                                                                                                                                                                                                                                                                                                                                                            Human genome
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23-SEP-1994
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            on 25-MAR-2003 to
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Starkey M;
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(first entry)
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' nontranslated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BYAT/)
(MATH/)
(TAON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            muscle deposition;
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11-JAN-2000; 2000US-0480902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine EST associated with lactation/muscle/fat deposition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAO N
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                                                                                                                                                                                                                                                                        SEQ ID No 5962; 245pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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Pred. No. 4.
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RESULT 11
ABI99762/c
ID ABI997
XX ABI997
XX ABI997
XX MOUSE;
XW MOUSE;
XW VASOSP
XX WUS MU
XX WO2001
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     WPI; 2002;034733/04
                                                  Ishikawa K,
                                                                                                                                                                                              18-MAY-2001; 2001WO-JP04192
                                                                                                                                                                                                                                                22-NOV-2001
                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                       Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse ischaemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABI99762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABI99762 standard; cDNA; 2152
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                                                                                                                                              18-MAY-2000; 2000JP-0145977
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                                                                                                 VIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                  Asai S,
                                                                                                 NIHON SCHOOL JURIDICAL
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71.9%;
                                                  Takahashi Y,
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Pred. No. 3.5
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                                                  Nagata T,
                                                                                                 PERSON
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in, a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB57020 to ABS57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB19914 represent pCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ABB57301.
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á 밁 Ş 멂 Ş B Š 뫄 S Best Local Similarity Matches 172; Conserv Query Match Sequence 2152 BP; 586 A; 455 C; 576 G; 535 T; 0 other; 1893 1953 2011 2070 660 601 541 421 AAGAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACTAATTACTGGCCAGCT 480 GTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGAAAACTCTTAAACTGAATCTTCAGC 540 ATAGTCAGCTTCATCAAGCACAGT 1870 ACAGTGATCCTCAAATATACTTCTAAGCAAAAC--AAGGGCTTTGTTTACTCAGTCTTCA NGAATAACCTTAAATATACTTTGTTAGCCAAAACCTTTTTTGTTTACATAGTTCTTT 600 GATTTTACTAGTTCTGAATTTTATTCTGAAACTCAAGTTTAACCCCCAAACCATCATTGAC 1894 GGATTTTTACTGTTCCTAATTTTATTCTGAAACTCCA-TTTTTCCCCCAGACCATAATTACC 659 CTATTTAACTTTGTTATGCACAGT - ATGGAAATCTGTTTCTTCTAGTCCCCCCAAGGAGAATGTCACACCGAGTGTCCAAC AACTATTAGTGAGAAACTGATGCAGGTAATTGAGTGTGAGGCACTAATTCCTGGTCAACT Conservative 12.5%; 0, Score 85.8; DB 24; Pred. No. 3.8e-06; 0; Mismatches 88; 683 Indels Length 2152; 4. Gaps 1954 2012 2071 ω

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RESULT 12
ABZ10246
ID ABZ10
XX ABZ10
AC ABZ10
XX I6-JA
CY Haema
XX Human
KW Human
KW Gytos
XX Homo
XX 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haematopoietic cell proliferation disorder related DNA sequence #386
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Human; haematopoietic cell proliferation gene therapy; lymphocytic leukaemia; acut 03-OCT-2002. WO200277272-A2 Homo sapiens cytosine methylation state; gene; ds. acute disorder; myelogenous leukaemia;

26-MAR-2002; 2002WO-EP03401

26-MAR-2001;

2001US-278333P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC differentiating between heamatopoietic cell proliferative disorders causpect. The method comprises contacting a trarget nucleic acid in a cc subject. The method comprises contacting a trarget nucleic acid in a cc biological sample obtained from the subject with at least 1 reagent, cc which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 cc dinvention. Oligonucleotides from the present invention. Oligonucleotides from the present for the present contacting between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the collanses. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between contact cell proliferation of haematopoietic cell proliferation of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olek A,
Lewin A,
Pelet C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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    Braun A, Distler J, Guetig D,
Piepenbrock C, Adorjan P, Grabs
Lipscher E, Maier S, Model F,
Schwope I, Ziebarth H;

                                                                                                                                                                                                                                                                                                                                                                                       TTTAANAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATNAATGCAGATAATTAAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTACATGAAAAAGTTAT--AACAAAGGACTGAGAACGTTATAAATTGAAATGAG 179
AAAATACTGTTTCTGATAGCATGAAATGCAAAATTTTTTAGATTTTTTAATCTCCCTAATTT
                                                                                                                                                                       GTGTTTTATGACTAATACACTGATTTTTCAATAAGGAAACCCATGTTAAAAAATATTTTTA 299
                                                                                                                                                                                                                                                                                                                                                              TTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCTATATCTCACTGAAT
                                                                                                                                                                                                                                               ATTATAATTTGAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATTATTCTTAATGATG 239
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     describes a method for detecting and en haematopoietic cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 71.6; DB 25; Pred. No. 0.00098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grabs G, Lesche
el F, Mueller V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Howe A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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ARESULT 13
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                                                               cc which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 crepresent specifically claimed nucleotide sequences from the present convention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative cd disorder haematopoietic cells; for differentiating between acute myelogenous leukaemia; as probes for complexity the cycosine methylation state and/or single nucleotide collymorphisms (SNPs) of haematopoietic cell proliferation disorder crelated sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation can complements; and as primers for the amplification of haematopoietic cell proliferation can complements; and as primers for the subclasses, diagnosis, prognosis, treatment and/or monitoring of chaematopoietic cell proliferation between subclasses, diagnosis, prognosis, treatment and/or monitoring of chaematopoietic classification of haematopoietic cell proliferative disorders. The present method enables can highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; haematopoietic cell proliferation gene therapy; lymphocytic leukaemia; acut cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for detecting and differentiating between haematopoletic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders, comprise that distinguishes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABZ10246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 28; SEQ ID 386; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2001; 2001US-278333P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002; 2002WO-EP03401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Braun A, Distler J, Guetig D, Piepenbrock C, Adorjan P, Grabs Lipscher E, Maier S, Model F, Schwope I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAGAACTATTGAGAAATTGATTAA 444
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Schwope I, Ziebarth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          describes a method for detecting
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e R, Leu E;
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Query Match

8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 other;

Score 70;

BB

25;

genomic

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RESULT 14
ABL70409
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Matches 320; Conservative
                                                                                                                                                                                                             Cell signalling; cytosine methylation; cell signalling
                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                         Chemically treated cell signalling
                                                                                                                                                                                                                                                                                                       01-JUL-2002
                     29-JUN-2001; 2001WO-EP07471
                                                                   10-JAN-2002.
                                                                                                           WO200202807-A2
                                                                                                                                                    Unidentified
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                                                                                   AGTAGAATAGTAT
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Pred. No. 0.0065;
0; Mismatches 220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7676 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid derived from chemically treated metastasis genes, useful for diagnosis of cancers by analysis of cytosine methylation, also for treatment -
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07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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Similarity 48.5%;
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                                                            GTTCAAGCTCTGATCATATTTCTTTTTTTTTTTTTTTTGGGAAGAAAATACTGTTTCTGATA 377
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10 US-09-998-598-578

10 US-09-998-598-578

10 US-10-102-524-161

10 US-10-102-524-161

10 US-10-102-524-188

14 US-10-102-524-645

16 US-09-960-352-5962

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                       Sequence 3296 Ap
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Sequence 27, Appl
Sequence 22, Appl
Sequence 161, App
Sequence 164, App
Sequence 645, App
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Sequence 3296, Ap
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US-09-835-992A-20

ALIGNMENTS

US-09-835-992A-20 Sequence 20, Application US/09835992A Patent No. US20020037541A1 GENERAL INFORMATION: APPLICANT: Obata, Yuichi TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED WITH GASTRIC CANCER ANI TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING GASTRIC CANCER FILE REFERENCE: L0461/7112 CURRENT APPLICATION NUMBER: US/09/835,992A CURRENT APPLICATION NUMBER: US/08/896,164 PRIOR APPLICATION NUMBER: US 08/896,164 PRIOR APPLICATION NUMBER: US 08/896,164 PRIOR FILING DATE: 1997-07-17 NUMBER OF SEQ ID NOS: 87 SOFTWARE: Patentin version 3.0 SEQ ID NO 20 NAME/KEY: Unsure LOCATION: (105)...(105) OTHER INFORMATION: n = a NAME/KEY: Unsure LOCATION: (412)...(412) OTHER INFORMATION: n = a FEATURE: NAME/KEY: Unsure LOCATION: (67)..(NAME/KEY: Unsure LOCATION: (541)..(541) OTHER INFORMATION: n = LENGTH: 687 TYPE: DNA ORGANISM: Homo sapiens OTHER INFORMATION: n = . (67) a, a v 9 ga Ca 'n ú 'n ç ω g ω ω õ ç e မ္ ct

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ATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCTATATCTCACTGAA 60

Query Match
Best Local Similarity 100.
Matches 687; Conservative

100.0%;

Score 683; DB 9; Lo Pred. No. 5.8e-114;

Length 687; Indels

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APPLICANT: Vockley, Joseph G.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Inc.
TITLE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3296
LENGTH: 1052
TYPE: DNA
COLUMN AND SERVICES
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FEATURE: OTHER INFORMATION: Genbank Accession No. US20020142981A1 U11313
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CURRENT APPLICATION NUMBER: US/09/835,992A; CURRENT FILING DATE: 2001-04-16; PRIOR APPLICATION NUMBER: US 08/896,164; PRIOR FILING DATE: 1997-07-17; NUMBER OF SEQ ID NOS: 87; SOFTWARE: Patentin version 3.0; SEQ ID NO 19; LENGTH: 714; TYPE: DNA
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                                                                                                                                      Sequence 19, Application US/09835992A
Patent No. US20020037541A1
GENERAL INFORMATION:
APPLICANT: Obata, Yuichi
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MO
TITLE OF INVENTION: METHODS FOR DIAGNOSING
FILE REFERENCE: L0461/7112
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Pred. No. 7.4e-106
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RESULT 4
US-09-796-692-7228
J Sequence 7228, Application US/09796692
Publication No. US20020198362A1
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FEATURE:
NAME/KEY: Unsure
LOCATION: (243)...(243)
OTHER INFORMATION: n = a.
NAME/KEY: Unsure
LOCATION: (373)...(373)
OTHER INFORMATION: n = a.
NAME/KEY: Unsure
LOCATION: (437)...(437)
OTHER INFORMATION: n = a.
NAME/KEY: Unsure
LOCATION: (702)...(702)
OTHER INFORMATION: n = a.
NAME/KEY: Unsure
LOCATION: (702)...(702)
OTHER INFORMATION: n = a.
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71; Conservative
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Pred. No. 4.1e-101;
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PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/22,903
PRIOR APPLICATION NUMBER: 60/22,903
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR PILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FRACTSCH FOR WINDOWS Version 3
SEQ ID NO 7228
LENGTH: 506
TYPE: DNA
ORGANISM: Homo sapiens
US-09-796-692-7228
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PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR PPLICATION NUMBER: 60/200,545
PRIOR PPLICATION NUMBER: 60/200,303
PRIOR PPLICATION NUMBER: 60/200,303
PRIOR PPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR PILING DATE: 2000-05-01
PRIOR PPLICATION NUMBER: 60/200,999
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-04
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Best Local S
Matches 471
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APPLICANT: Galger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
393
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Similarity 99.4%;
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Q for Windows Version
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Pred. No. 8.8e-76;
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; ORGANISM: Homo sapiens
US-10-040-862-7228
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US-10-040-862-7228
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Best Local Similarity
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Publication No. US20030078396A1
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SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
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CURRENT FILING DATE: 2001-11-06
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APPLICANT: Retter, Marc
APPLICANT: Corix Corporation
APPLICANT: Corix Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection,
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
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FILING DATE: 2000-04-27
APPLICATION NUMBER: US 60/200,303
FILING DATE: 2000-04-28
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APPLICATION NUMBER: US 60/218,950
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APPLICATION NUMBER: US 09/796,692
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APPLICATION NUMBER: US 60/223,416
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                                                                                                          ACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAAATTGAAATGAGA
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Pred. No. 8.8e-76;
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US-09-998-598-578
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APPLICANT: Stolk, Joi
APPLICANT: Xu, Jian
APPLICANT: Chenault
APPLICANT: Meagher,
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SOFTWARE: Corixa Invention
SEQ ID NO 578
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APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FO
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
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Pred. No. 3.3e-75;
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TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLE
TITLE OF INVENTION: METHODS FOR DIAGNOSING AN
FILE REFERENCE: L0461/7112
CURRENT APPLICATION NUMBER: US/09/835,992A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 08/896,164
PRIOR PILING DATE: 1997-07-17
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
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Patent No. US20020037541A1
GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                   NAME/KEY: Unsure
LOCATION: (80)..(80)
OTHER INFORMATION: n
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LOCATION: (74)..(74)
OTHER INFORMATION: n
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LOCATION: (33)..(33)
OTHER INFORMATION: n
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LOCATION: (92)..(93)
OTHER INFORMATION: n
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LOCATION: (56)..(56)
OTHER INFORMATION: n
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LOCATION: (42)..(42)
OTHER INFORMATION: n
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LOCATION: (19)..(19)
OTHER INFORMATION: n
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LOCATION: (95)..(95
OTHER INFORMATION:
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OTHER INFORMATION: n
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OTHER INFORMATION: n
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LOCATION: (69)..(69)
OTHER INFORMATION: n
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LOCATION: (64)..(65)
OTHER INFORMATION: n
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OTHER INFORMATION: n
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LOCATION: (47)..
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NAME/KEY: Unsure
LOCATION: (122)...(122)
OTHER INFORMATION: n = a
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LOCATION: (249)..(249)
OTHER INFORMATION: n =
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LOCATION: (229)..(229)
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LOCATION: (255).
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APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
FILE REFERENCE: 210121.572
CURRENT APPLICATION NUMBER: US/10/102,524
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 1863
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 161
LENGTH: 510
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                                                           CTGTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGAAAACTCTTAAACTGAATCTTCA
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Gaiger, Alexander
                                                                                                                             23.6%;
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                                                                                                          Score 161.8; DB Pred. No. 5e-20; 0; Mismatches
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APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane
APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Alexander
APPLICANT: Gordon, Brian
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF K.
FILE REFERENCE: 210121.572
CURRENT APPLICATION NUMBER: US/10/102,524
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEO ID NOS: 1863
SOFTWARE: FASTSEQ for Windows Version 4.0
SEO ID NO 188
LENGTH: 510
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Alexander
APPLICANT: Gordon, Brian
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF K.
FILE REFERENCE: 210121.572
CURRENT APPLICATION NUMBER: US/10/102,524
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 1863
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-102-524-645
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US-10-102-524-188/c
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; ORGANISM: Homo
US-10-102-524-188
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Publication No. US20030109434A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Publication No. US20030109434A1
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Best Local Similarity
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Patent No. US20020137139A1

Patent No. US20020137139A1

REPLICANT: Warren, Weeley C.
APPLICANT: Warren, Weeley C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10299) C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 5962

LENGTH: 397

TYPE: DNA

ORGANISM: Bos taurus

OTHER INFORMATION: Clone ID: 26-LIB188-014-Q1-E1-G5
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; ORGANISM: Homo sapiens
US-10-102-524-645
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US-09-960-352-5962
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LENGTH: 510
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Best Local Similarity
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                          TA-TTAACTTTGTAATGCACAGTTGTT
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Pred. No. 1.4e-09;
0; Mismatches 65; Indels 10;
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RESULT 13
US-10-311-455-2147/c
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US-10-240-485-151
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US-10-240-485-151
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PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
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Best Local Similarity
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SEQ ID NO 151
LENGTH: 7676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Diagnosis of Diseases Associated with TITLE OF INVENTION: Metastasis FILE REFERENCE: 5013.1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/240,485
CURRENT FILING DATE: 2002-10-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OLEK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                            TATATTAATTATTATATAAATAAATATAAGATATGAAATATTTAAGAAATTGAAAAGTTT 3816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTCTTCTCAAAGCATTATTTTATCCTATATCTCACTGAATTTAANAAATAACATT--- 77
                                                                                                                                                       AAATAGTAATTATTTTTTTTTTTTTTTTTTTTTTATTAGTAATAGTAAATTTTAGAGATT 4116
                                                                                                                                                                                        GCATGAAATGCAAAATTTTTAGATTTTTAATCTCNCTAATTTTAAGAACTATTGAGAAAT 437
                                                                                                                                                                                                                                                                                                                 ACTGATTTTTCAATAAGGAAACCCATGTTAAAAAATATTTTTATTTTAAAAAATAAGGCCTGT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                AGTATTAGAAAAACTAGGAAAAAAGATNAATGCAGATAATTAAACTTACATGAAAAAGGA 137
                                                                                                                                                                                                                          TTTTTTGGTGTGTTTTTTTTTTTTTGAAATATTTTTTGTTTGAAATTAAATTTAGTTTTA
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Pred. No. 0.016;
0; Mismatches 220;
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; OTHER INFORMATION: chemically treated US-10-311-455-2147
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: DCT/EP01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PRIING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2147
FENCETT- 1115-15
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Best Local Similarity
Matches 282; Conser
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ORGANISM: Artificial Sequence
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                                                                                                                                               TAACCTTAAATATACTTTGTTAGCCAAACAAAACTTTTTTGTTTACATAGTTCTTTGGAT
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                                              TTTACTGTTCCTAATTTTATTCTGAAACT 633
                                                                                                                                                                                                                                             GCATTGTGTTTCTTACTTAGTTCTCCCCAAGGAAAACTCTTAAACTGAATCTTCAGCNGAA
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Pred. No. 0.083;
0; Mismatches 344
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APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: HOR IDENTIFICATION, ASSESSMENT, PRI
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: 807, 808, 819, 820, 821, LOCATION: 871, 874, 875, 891, 892, LOCATION: 917, 923, 925, 926, 927, OTHER INFORMATION: n = A,T,C or G US-10-198-846-6381
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US-10-198-846-6381/c
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Best Local Similarity
Matches 199; Conserv
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TYPE: DNA
ORGANISM: Homo Bapiens
FENTURE:
NAME/KEY: misc_feature
LOCATION: 1, 8, 66, 71,
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                             TGGGAAGAAAATACTGTTTCTGATAGCATGAAATGCAAAATTTTTTAGATTTTTAATCTCN 412
                                                               AANNTTTTNTAANTTATTAAACCAAAATTTTTTTTTTAAAAATTTTTTTAAAANTTAAT
TTTAAAAAAAANNTTTTTTTTTTTATANTTTATAAAAATTTTATTTNTNTTTTTCTNA
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Pred. No. 0.034;
0; Mismatches 273;
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PREVENTION,
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GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: PIEPENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the

FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: DET1032529.7

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NO 1445

SEQ ID NO 1445

LENGTH: 6106
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US-10-311-455-1445/c
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Publication No. US20030143606A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 198; Conserv
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Best Local
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      ACAACA 463
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Pred. No. 0.073;
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ATAATA 2713

Search completed: November 27, 2003, 12:52:57 Job time : 263.057 secs

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Result
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-641-638-651
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Sequence 22, Appl
Sequence 1553, Ap
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ALIGNMENTS

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RESULT 1
US-08-896-164-20
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MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,164
FILING DATE: July 17, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6218521man D. Hanson
REGISTRATION UNMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5499
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 638-3884
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application of the patient No. 6218521 general INFORMATION: GENERAL INFORMATION: ISOL
                                                                                                                    Query Match
Best Local Similarity
Matches 687; Conserv
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TITLE OF INVENTION: USOLATED NUCLEIC ACID MOLECULES ASSOCIATED
TITLE OF INVENTION: WITH GASTRIC CANCER AND METHODS FOR
TITLE OF INVENTION: DIAGNOSING AND TREATING GASTRIC CANCER
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felie & Lynch
                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 687 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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New York City
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  TTTTAANAAATAACATTAGTATTAGAAAAACTAGGAAAAAGATNAATGCAGATAATTAA 120
                                        ATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCTATATCTCACTGAA
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                                                                                                                                       99.4%; Score 683; DB 3; 100.0%; Pred. No. 1.5e-1
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                                                                                                                      Mismatches
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RESULT 2
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Patent No. 6218521

GENERAL INFORMATION:
APPLICANT: OBATA, Yuichi
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED
TITLE OF INVENTION: WITH GASTRIC CANCER AND METHODS FOR
TITLE OF INVENTION: DIAGNOSING AND TREATING GASTRIC CANCER
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
                            COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/89
FILING DATE: July 17, 1997
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
ATTORNEY/AGENT INFORMATION:
NAME: No. 6218521man D. 1
REGISTRAȚION NUMBER: 30,
                                                                                                                                                  STREET:
CITY: Ne
STATE: N
COUNTRY:
ZIP: 100
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New York City
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                 Sequence 22, Application Patent No. 6218521 GENERAL INFORMATION:
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APPLICANT: OBATA, Yuichi
TITLE OF INVENTION: ISOL
TITLE OF INVENTION: WITH
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ISOLATED NUCLEIC ACID MOLECULES WITH GASTRIC CANCER AND METHODS
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Pred. No. 3.4e-115;
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INFORMATION FOR SEQ ID NO: 22
SEQUENCE CHARACTERISTICS:
LENGTH: 843 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity
Matches 495; Conserv
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
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NAME: NO. 6218521man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5499 - JEL/NDH/SLH
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OPERATING SYSTEM: PC-DC
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
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FILING DATE: July 17, 1997
CLASSIFICATION: 424
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                                                                                             AAGAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACTAATTACTGGCCAGCT 480
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Pred. No. 6.8e-75;
O; Mismatches 190;
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FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6476212 700551132H1

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US-09-313-294A-1553/c
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                                                                                                                                                                                                                                                                                 Sequence 2, Application Patent No. 5389526 GENERAL INFORMATION:
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SOFTWARE: PERL Progra
SEQ ID NO 1553
LENGTH: 173
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Best Local Similarity
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APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcook Washburn Kurtz Mackiewicz STREET: One Liberty Place 46th Floor
                                                                                                                                                                  APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors I
TITLE OF INVENTION: Slime Moulds of the Genus
NUMBER OF SEQUENCES: 19
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                        STATE: F
                                                                                               CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 TTTÄÄTTTTCTÄTTAAACATTCTTCTCÄÄAGCATTATTTTATCCTÄTATCTCÄCTGAATT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  554 AAAATAACCCTTAANTATCCTTGGTAACCAAANCAAAACCTTTTTNGTTTACNTANTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAANAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATNAATGCAGATAATTAAAC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCTATATCTCACTGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTATTTAACTTTGTTATGCACAGTTGTT 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTAAGAAATAACATTAGTATTAGAAAAAACTAGGAAAAAAGATAAATGCAGATAATTAAAC
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Pred. No. 2e-24;
0; Mismatches 2; Indels
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OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

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; FEATURE:
; NAME/KEY:
; LOCATION:
US-07-867-106-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 46.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNALICATION NUMBER: 35,134
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE
TELECOMMUNICATION INFORMATION:
TOTREPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOPTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,10
FILING DATE: 19920625
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
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APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5691
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                                        478 GCTGTTGGCATTGTGTTTCTTACTTAGTTCTCC 510
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AATGGATACTAGATCCTTTTTCCCAAGTTTTCC 5239
                                                                                                                                                                   TAAATTTAATATTTAAATTTTAAAAATTAGTGATCTATCGATCTATAAATTTTCCATG 533
                                                                                                                                                                                                            AGAAAATACTGTTTCTGATAGCATGAAATGCAAAATTTTTTAGATTTTTAATCTCNCTAAT 417
                                                                                                                                                                                                                                                                                                                                                                           GTTTTATGACTAATACACTGATTTTTCAATAAGGAAACCCATGTTAAAAATATTTTTATT 301
                                                                                                                                                                                                                                                                                                                                                                                                                    TAAAAAATGTAAAGGGTTTTTTTTAAAAATTATGTATCGATTTTTATTTTAAAATCATTGA 5512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCTATATCTCACTGAAT 61
                                                                                                                          TTTAAGAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACAACTAATTACTGGCCA 477
                                                                                                                                                                                                                                                     TTTTTAÄAAATTCAAATAATTAAATTATCTATATCTTGATGAACTTCAATTTTTA
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                                                                                   TTTTTAAAATTTTTTTAAAGTATTTTTTTAATTAATAGTACTGCACGGATTAATATGGA
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2378..5038
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Pred. No. 3.2e-05;
0; Mismatches 269;
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TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENEST.051CP1
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILLING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 09/133,200
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-03
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 651
LENGTH: 20674
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LOCATION: 16567..16667
OTHER INFORMATION: exon 12
NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon 13
                                                                                                                                             LOCATION: 13308..13429
OTHER INFORMATION: exon
NAME/KEY: exon
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OTHER INFORMATION: exon 10
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                                                                                                                                                                                                                               NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                               LOCATION: 12254..12340
OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
NAME/KEY: exon
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LOCATION: 5552..5633
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
NAME/KEY: exon
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LOCATION: 1123..3123
OTHER INFORMATION: 5'regulatory
NAME/KEY: exon
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Chumakov, Ilya
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OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 4088
OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 4109
OTHER INFORMATION: 1
NAME/KEY: allele
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NAME/KEY: allele
LOCATION: 2934
OTHER INFORMATION:
NAME/KEY: allele
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NAME/KEY: allele
LOCATION: 2832
OTHER INFORMATION: 10-513-250
NAME/KEY: allele
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LOCATION: 1827
OTHER INFORMATION:
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                       OTHER INFORMATION: NAME/KEY: allele LOCATION: 6183
                                                                                                              OTHER INFORMATION:
NAME/KEY: allele
                                                                                                                                       OTHER INFORMATION: NAME/KEY: allele LOCATION: 5903
                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
NAME/KEY: allele
LOCATION: 4062
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LOCATION: 2623
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NAME/KEY: allele
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OTHER INFORMATION:
NAME/KEY: allele
                                                             NAME/KEY: allele
LOCATION: 6141
                                                                                       OTHER INFORMATION:
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LOCATION: 3802
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                                                                                                     COCATION: 6019
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             10-346-305
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OTHER INFORMATION: 1
NAME/KEY: allele
NAME/KEY: 8777
TON: 8777
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LOCATION: 12429
OTHER INFORMATION: 10-350-332
NAME/KEY: allele
LOCATION: 13341
OTHER INFORMATION: 10-507-170
NAME/KEY: allele
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OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 13524
OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 13535
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OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 8926
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NAME/KEY: allele
LOCATION: 12171
OTHER INFORMATION: 1
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LOCATION: 6611
OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 7668
OTHER INFORMATION: 1
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NAME/KEY: allele
LOCATION: 6484
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LOCATION: 8658
OTHER INFORMATION: 10-349-97
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LOCATION: 8608
OTHER INFORMATION: 10-349-47
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NAME/KEY: allele
LOCATION: 6375
OTHER INFORMATION: 10-347-111
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                    GAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAAATTGAAATGAGATTATAATT
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                                                                                             APPLICATION NUMBER: CH 0016/9
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-441-8587
                                                                      TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                         SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                APPLICATION NUMBER:
             STRANDEDNESS:
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Research Triangle Park
No. 6239264th Carolina
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VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
VENTION: AND USES THEREOF
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Knechtle, Philipp
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Steiner, Sabine
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31-DEC-1996
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APPLICANT: Lynn DOUGETTE-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACITITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOST FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR PRICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 150

LENGTH: 927
                                      US-09-134-001C-150
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                                                                                                                                                                                                                                                                                                                                        Sequence 150, Application US/09134001C Patent No. 6380370
   Query Match
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Best Local
                                               TYPE: DNA ORGANISM: Staphylococcus epidermidis
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAAATTGAAATGAGA 180
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45.6%;
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   Score 53.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 53.6; DB Pred. No. 0.01;
                                                                                                                                                                                                                                                                 AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS DIAGNOSTICS AND THERAPEUTICS
   DB
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   4.
Length 927;
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RESULT 9
US-08-998-416-186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                          TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic scid
                                                                                                                                            CLASSIPICATION: 435
PRIOR APPLICATION NUMBER: CH 0016/9
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERRNCE/DOCKET NUMBER: PF/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQU
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                               STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997
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o. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEB: No. 6239264artis Corporation
T: 3054 Cornwallis Road
Research Triangle Park
: No. 6239264th Carolina
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Steiner, Sabine
Mohr, Christine
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                               lineau
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             DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                  Version
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US-09-056-075-1
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Patent No. 5955368
GENERAL INFORMATION:
APPLICANT: Johnson, Eric A.
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Best Local Similarity
Matches 213; Conserv
                                                                                                                                             COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                           ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rood, JU
TITLE OF INVENTION:
TITLE OF INVENTION:
TELECOMMUNICATION INFORMATION: TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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CITY: Madison
                                REFERENCE/DOCKET NUMBER:
                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                  STATE:
                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 ACTTTTTTATTATATATATTTAAGTATTAATTATTTAAACTATTATTATTATTTAAT 101
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                                                                                                                                                                                                                                                                                                                  E: Quarles & Brady
1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                  Bradshaw, Ma
Rood, Julian
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45.9%;
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RESULT 11
US-08-998-416-186/c
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SEQUENCE CHARACTERISTICS:
LENGTH: 6243 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                           Sequence 186, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 46.8 Matches 191; Conservative
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                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Philip
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                              APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                         ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina
                                                        COUNTRY: U
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 3770..4013
OTHER INFORMATION: /note= "RP4 origin of DNA transfer
OTHER INFORMATION: plasmid RP4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAATGAGCCTTTATAAAAGCCCATTTTTTTCATATACGTAATATGACGTTCTAATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTTGAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATTATTCTTAATGATGGTGTT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAAATTGAAATGAGATTAT 184
                                                                       USA
                                                                                                                                                                                                                                                                                                      Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                   Wendland, Jurgen
Knechtle, Philipp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.5%;
Local Similarity 46.5%;
les 265; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241 REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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   AGCNGAATAACCTTAAATATACTTTGTTAG
                                                              GCTGTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGAAAACTCTTAAACTGAATCTTC 537
                                                                                            AAGAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACT---AATTACTGGCCA
                                                                                                                                                                                    AAATACTGTTTCTGATAGCATGAAATGCAAAATTTTTTAGATTTTTAATCTCNCTAATTTT 420
                                                                                                                                                                                                                                               TTTAAAAATAAGCCTGTGTTCAAGCTCTGATCATATTTCTTTTATTTTGATTTGGGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCTATATCTCACTGAATTTTA
                                 AGAAAATAATATCTAATAATATTTTAATAACTAATTTAAAATTTGAACATAGACTAA
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RESULT 13
US-08-213-419B-3/c
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SEQ ID NO 63
LENGTH: 1692
TYPE: DNA
ORGANISM: Ureaplasma urealyticum
5-09-601-198-63
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Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Inselbu
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Best Local Similarity
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                                                                                                       SOFTWARE:
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APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
TITLE OF INVENTION: UREALYTICUM
FILE REFERENCE: UAB-13452/2
CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/073,189
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181
                                                                                                                                                           APPLICANT: Inselbirg, J. et al.

TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM TITLE OF INVENTION: AND USES THEREFOR FILE REFERENCE: JII-002CNCP CURRENT APPLICATION NUMBER: US/08/213,419B CURRENT FILING DATE: 1994-03-14 PRIOR APPLICATION NUMBER: US/0870,506 PRIOR PILLORIUM NUMBER: US/087
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APPLICANT: Chen, E
APPLICANT: Glass,
ORGANISM: Plasmodium falciparum
                                 TYPE: DNA
                                                           ENGTH: 6124
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                                                                                                                                     PatentIn Ver. 2.0
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Elleon Y.
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RESULT 14
US-08-998-416-1137/c
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NAME/KEY: CDS
NAME/KEY: CDS
LOCATION: (2598)...(3404)
NAME/KEY: CDS
LOCATION: (3580)...(3720)
NAME/KEY: CDS
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NAME/KEY:
LOCATION:
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Pred. No. 0.06;
                                                                                                                                                               TTTTTTTTTTGTTATATTATTT 5838
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Patent No. 623926
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                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0
FILING DATE: 31-DEC-1996
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ATTORNEY/AGENT INFORMATION: NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                  USA
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Knechtle, Philipp
Rebischung, Corinne
Rebischung, Corinne
Rebischung, Corinne
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Steiner, Sabine
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                                                          CH 0016/97
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RESULT 15
US-08-487-826B-13
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                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Sim, K
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1137
                                                        APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Su, Xin-Zhaun
APPLICANT: Su, Xin-Zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE |
                              NUMBER OF SEQUENCES: 4
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ORIGINAL SOURCE:
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LENGTH: 636 base pairs
TYPE: nucleic acid
                ADDRESSEE:
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240; Conserv
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E: Knobbe Martens Olson & 620 Newport Center Drive
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16th Floor
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Best Local Similarity 45.7%;
Matches 200; Conservative
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INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: lir
MOLECULE TYPE:
HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/487,826B FILING DATE: 10-SEP-1993 CLASSIFICATION: 435
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STATE: California
COUNTRY: US
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2176
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                              AATTGATTAATGACATGA 452
                                                                                                                                   TTÄATCGTATGACATAAAATTATATTATATTAGAAATTAAAATTCAAAATTATAAAAAAT 1936
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                                                              ATAGCATGAAATGCAAAATTTTTAGATTTTTAATCTCNCTAATTTTAAGAACTATTGAGA 434
                                                                                                                                                                   TGTGTTCAAGCTCTGATCATATTTCTTTTATTTTGATTTGGGAAGAAAATACTGTTTCTG
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Pred. No. 0.14;
0; Mismatches 237;
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Search completed: November Job time: 51.7082 secs

27, 2003, 12:32:17

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Minimum DB seq
Maximum DB seq
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AR146581	RESULT 1
methods for diagnosing and treating gastric cancer Patent: US 6218521-A 21 17-APR-2001;	Isolated nucleic acid molecules associated with gastric cancer and	Obata, Y.	1 (bases 1 to 994)	Unclassified.	Unknown:	Unknown:		AR146581.1 GI:15109770	AR146581	Sequence 21 from patent US 6218521.	AR146581 994 bp DNA linear PAT 08-AUG-2001		

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Homo sapiens

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 994)

5 Old, L.J., Scanlan, M.J., Stockert, E., Gure, A., Chen, Y.T., Gout

OGhare, M., Obata, Y., Pfreundschuh, M., Tureci, O. and Sahin, U.

Cancer-associated nucleic acids and polypeptides

Patent: JP 2001516009-A 496 25-SEP-2001;

LDUBWIG INSTITUTE FOR CANCER RESEARCH

OS Homo sapiens (human)

PY 2001516009-A/496

PD 25-SEP-2001

PF 15-JUL-1998 JP 2000503425

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A61P35/00,
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C07K14/82,C07K16/32,C12N15/09//C07K16/46,C12P21/08,A61K37/02,
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Cancer-associated nucleic acids and polypeptides. FH Key
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PR 17-JUL-1997 US 60/061765,10-OCT-1997 US 08/948705 PR
10-OCT-1997 GB 9721697.,22-JUN-1998 US 09/102322 PI
JOLD, MATTHEW J SCANLAN, ELISABETH STOCKERT, ALI GURE, YAO PI
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re,Z., Yamamoto,R., Furth,E.E., Schantz,L.J., Naylor,S.L., George,H., Billheimer,J.T. and Strauss,J.F. III. cDNAs encoding members of a family of proteins related to human sterol carrier protein 2 and assignment of the gene to human chromosome 1 p21---pter DNA Cell Biol. 10 (8), 559-569 (1991) 92029618
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Query Match
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Matches 897; Conserv
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On Dec 6, 1993 this sequence version replaced
Original source text: Human liver cDNA to mRNA
Location/Qualifiers
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                                                                                                                                                                                    GAACAAAAATTGAACACTTTGCAAAAATTGGATGGAAAAATCATAAACATTCAGTTAATA
                                   ACCCGTATTCCCAGTTCCAAGATGAATACAGTTTAGATGAAGTGATGGCATCTAAAGAAG
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ACCCGTATTCCCAGTTCCAAGATGAATACAGTTTAGATGAAGTGATGGCATCTAAAGAAG
                                                                                                                                                 GAACAAAATTGAACACTTTGCAAAAATTGGATGGAAAAATCATAAACATTCAGTTAATA
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//db xref="G1:432975"
//db xref="G1:43297
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2258. .2263
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/evidence=experimental
439 c 570 g
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/db_xref="taxon:9606"
/map="1p32"
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/evidence=experimental
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/codon_start=1
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/clone_lib="Clontech HL-1001b;HL-1115b"
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Weber, F.E., Werder, M., Boffelli, D. and Hauser, H. In pre-sterol carrier protein 2 (SCP2) in solution the leader peptide 1-20 is flexibly disordered and the residues 21-143 ac
                                                    Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 2661)
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Oryctolagus cuniculus sterol
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Submitted (02-MAR-1998) Kieferchirurgie,
Raemistr. 100, Zurich 8991, Switzerland
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Unpublished
2 (bases 1 to 2661)
Weber, F.E., Werder, M.,
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CTTATGAAGCACTGGGACTCTGTCCAGAAGGACAAGGTGCAACGCTGGTTGATAGAGGAG
                                                        GACCAAGTGATATTGATGTAATAGAACTTCATGATTGCTTTTCTGCCAACGAACTCCTCA
                                                                             CACCAAATGATATTGACGTAATAGAACTTCACGATTGCTTTTTCTACCAACGAACTCCTTA
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53. .1696
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/mol_type="mRNA"
/db_xref="taxon:9986"
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1. .2661
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/protein_id="AAC15422.1"
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The amino acid sequence of rat liver non-specific lipid protein (sterool carrier protein 2) is present in a high weight protein: evidence from cDNA analysis
Biochem. Biophys. Res. Commun. 168 (2), 631-636 (1990)
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Mammalia; Eutheria; Rodentia;
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/protein id="nan41726.1"
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VNNPYSQGFQDEYSLLDEIMKSREPVEFLTVLQCCPTSDGAAAAIVSEEFVQKHGLQSK
VNNPYSQGFQDEYSLLDEIMKSREPVEFLTVLQCCPTSDGAAAAIVSEEFVQKHGLQSK
AVEIVAQEMVTDMPSTFEEKSVIKMVGYDMSKEAARKCYEKSGLGPSDVDVIELHDCF
STNELLTYEALGCLCPEGQGGALVUNGGDAVVTLYRMGFPEAASSFRTHGISAAPT
SSAGDGFKANLIFKEIEKKLEEEGEEFVKKIGGIFAFKVKDGPGGKEATWVVDVKNGK
GSULPDSDKKADCTITMADSDLLALMTGKMNPQSAFFQGKLKIAGNMGLAMKLQSLQL
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/mol_type="mRNA"
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issue_type="liver"
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                                                                        TGAAAGAAAAATNCGGNGGGAATTTTTTGCCCTTCAAGGGGAAAAAAATGGCCCTTGGGGGGT
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                                                                                                                                                                                                                                                                                                                                                                              4 (bases 1 to 1945)
Ossendorp,B.C.
Direct Submission
Submitted (03-JUL-1991) B.C. Ossendorp,
Lipid, Enzymology, State, University of
3508 TB Utrecht, THE NETHERLANDS
See also M58287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ossendorp, B.C., Van Heusden, G.P., De Beer, A.L., Bos, K., Schouten, G.L. and Wirtz, K.W. Identification of the cDNA clone which encodes the 58-kDa proteir containing the amino acid sequence of rat liver non-specific lipid-transfer protein (sterol-carrier protein 2). Homology with rat peroxisomal and mitochondrial 3-oxoacyl-CoA thiolases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol.
91093192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning, expression, and nucleotide sequence carrier protein 2 cDNAs
J. Biol. Chem. 266 (1), 630-636 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Characterization of a cDNA encoding rat DNA Cell Biol. 9 (3), 159-165 (1990) 90253610
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non-specific lipid transfer
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Mammalia; Eutheria; Rodentia;
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            LFG$AGKEHMETYGTKVEHFAKIGWKNHKHSVNNPYSQFQDEYSLDEIMKSRPVFDFL
TVLQCCPTSDGAAAIVSSEEFVQKHGLQSKAVEIVAQEMVTDMPSTFEEKSVIKMVG
YDMSKEAARKCYEKSGLGPSDVDVIELHDCFSTNELLITYEALGLCPEGQGGALVDRGD
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/tranalation="PSVALNSPRLRRVEVVGVGMTKFMKPGGENSRDYPDLAKEAGQK
/tranalation="PSVALNSPRLRRVEVVGVGMTKFMKPGGENSRDYPDLAKEAGQK
ALADRQIPYSANEQACYVGESTGLFM
AQQLVQGGLANCVLALGFEKMEKGSLGTKYSDRSNPLEKHIDVLINKYGMSACPFAPQ
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                                                                                                            /codon_start=2
/protein_id="CAA43061.1"
/db_xref="GI:56773"
                                                                                                                                                          /note="open reading frame for 58 kDa protein containing
the non-specific lipid transfer protein"
NTYGGKWVINPSGGLISKGHPLGATGLAQCAELCWQLRGEAGKRQVPGAKVALQHNLG
                                                                                                                                                                                                                              /tissue_type="liver"
/clone_lib="lambda_gi
/dev_stage="adult"
                                                                                                                                                                                                                                                                                         /strain="sprague-dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                   organism="Rattus norvegicus"
                                                                                                                                                                                                      /evidence=experimental
                                                                                                                                                                                                                                                                              'sex="Female"
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GKMNPQSAFFQGKLKIAGNMGLAMKLQSLQLQPDKAKL"
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/note="non-specific lipid transfer protein presequence"
1415 c 535 g 464 t
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EEFVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPDSDKKADCTITMADSDLLA
LMTGKMNPQSAFFQGKLKIAGNMGLAMKLQSLQLQPDKAKL"
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/protein_id="CAA43060.1"
/db_xref="GI:56772"
/db_xref="SWISS-PROT:P11915"
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                                                                                                                                                               Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 42 Row: n Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., García, A.M., Lu, X., Hulyk, S.W.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey |
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1980 bp mR
Mus musculus, sterol carrier protein
IMAGE:5123611, mRNA, complete cds.
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Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1980)
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/organism="Mus musculus"
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AAGCCGGAAAAGAGCCAAAGTTCCTGGTGCAAAGGTGGCTCTGCNGCATAATTTANGCAT
                                                       ACCCACTGGGCGCAACAGGTCTGGCTCAGTGCGCGGAGCTCTGCTGGCAGCTGAGAGGCG
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PVKKIGGIFAFKVKDGPGGKEATWVDVKNGKGSVLPNSDKKADCTITMADSDLLALM
TGKMNPQSAFFQGKKLTAGNMGLAMKLQNLQLQPGKAKL"

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/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
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0; Mismatches 184;
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                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LIAN, at; http://image.llnl.g Series: IRAK Plate: 17 Row: n Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly;
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart.
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Center code: BCM-HGSC
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/clone="MGC:11534 IMAGE:3710340"
/tissue_type="Mammary tumor. C3(1)-Tag model.
ductal carcinoma. 5 month old virgin mouse."
                                                                                              organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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/protein_id="AAH18384.1"
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/lab_host="DH10B"
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Seedorf, U., Raabe, M. and Assmann, G.
Seedorf, U., Raabe, M. and Assmann, G.
Cloning, Expression, and Nucleotide Sequence of Mouse Sterol
Carrier Protein x cDNAs and Structure of a Related Pseudogene
Unpublished (1992)
Original source text: R.norvegicus (strain Wistar) adult lives
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Schooling, expression, and nucleotide sequence carrier protein 2 cDNAs
J. Biol. Chem. 266 (1), 630-636 (1991)
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M57453.1 GI:206876
alternative splicing; sterol carrier protein.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eutus norvegicus
Eutaryota, Metazoa; Chordata; Craniata; Vertebrata; E
Eukaryota, Metazoa; Chordata; Sciurognathi; Muridae;
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                                                                                                                                                                                                                       /organism="Rattus norvegicus"
/mol type="mRNA"
/strain="Wistar"
/db xref="taxon:10116"
/tissue_type="liver"
/dev stage="adult"
           /codon start=1
/product="sterol carrier protein-x"
/protein id="AAAA42122:1"
/db_xref="GI:206877"
                                                              'gene="SCP-2"
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                                                                                                      product="2.1 kb mRNA"
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                                                                                                                                            evidence=experimental
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'translation="MPSVALNSPRLPRVFVVGVGMTKFMKPGGENSRDYPDLAKEAGQ
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                          GAACGCACCAGATTTCA---GCTGCTCCCACCAGCTCTGCAGGGGATGGATTCAAGGCAA
                                                                                              GAACTGTGGTTGTAACACTCTACAAGATGGGGTTTTTCCCGGAAGCCGCCAGTTCCTTTTA
                                                                                                                                 GGAAA--GAGGCAGGTTCCTGGGGCAAAGGTGGCTCTGCAGCACAATTTAGGCCTTGGAG
                                                   GAACTCATCAAAATTGAAGCCNGTTCCAACCAAGCTCTGCAAGTNATNGGTTTAANGNAA 845
                                                                               GAGCTGCTGTTGTCACCCTCTACAGAATGGG--TTTTTCCCGAAGCTGCCAGCTCC-TTCA
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KALADROI PYSAVEQACVGYVYGESTCGQRAIYHSLGLTGI PIINVNNNCSTGSTALF MAQQLVQGGLANCVLALGFEKMEKGSLGTKYSDRSNPLEKHI DVLINKYGMSACPFAP QLFGSACKEHMETYGTKVEHFAKIGWKNHKHSVNNPYSQFQDEYSLDEIMKSRPVFDF LTVLQCCPTSDGAAAAIVSSEEFVQKHGLQSKAVEIVAGENVTDMPTTFEEKSVIKMV GYDMSKEAARKCYEKSGLGPSDVDU ELHDCFSTNELLTYEALGLCPEGQGGALVDRG DNTYGGKWVINPSGGLISKGHPLGATGLAQCAELCWQLRGEAGKRQVPGAKVALQHNL GLGGAAVVTLYRMGFPEAASSFRTHQISAAPTSSAGDGFKANLIFKEIEKKLEEEGEE FVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPDSDKKADCTITMADSDLLALM TGKMNPQSAFFQGKLKIAGNMGLAMKLQSLQLQPDKAKL" ი ω

Similarity GAAGCACTGGGACTCTGTCCAGAAGGACAAGGTGCAACGCTGGTTGATAGAGGAGATAAT GGCTTTGATATGAGTAAAGAAGCTGCAAGAAATGCTATGAGAAATCTGGCCTGACACCA GCCAGTGAAGCATTTGTACAGAAGTATGGCCTGCAATCCAAAGCTGTGGAAATTTTTGGCA TATTCCCAGTTCCAAGATGAATACAGTTTAGATGAAGTGATGGCATCTAAAGAAGTTTTT AAAATTGAACACTTTGCAAAAATTGGATGGAAAAATCATAAACATTCAGTTAATAACCCG CCAGTTGCTCCTCAGATGTTTGGGTATGCTGGAAAAGAACATATGGAAAAATATGGAAACA ACATATGGAGGAAAGTGGGTCATAAATCCTAGTGGTGGACTGATTTCAAAGGGACACCCA CAAGAAATGATTACTGATTTGCCAAGCTCGTTTGAAGAAAAAAGCATTATTAAAATGGTT GATTTTTTGACTATCTTACAATGTTGTCCCACTTCAGATGGTGCTGCAGCAGCAATTTTG CCATTTGCTCCTCAGCTGTTTGGGAGCGCTGGGAAAGAACATATGGAAACATATGGAACA CTGGGTGCCACAGGTCTGGCTCAGTGCGCGGAGCTCTGCTGGCAGCTGAGAGGCGAAGCC CTAGGCGCTACAGGTCTTGCTCAGTGTGCAGAACTCTGCTGGCAGCTGAGAGGGGAAGCC ACTTACGGAGGAAAGTGGGTCATAAAACCCTAGTGGAGGCCTCATCTCCAAGGGACACCCA GAAGCACTGGGGCTCTGTCCAGAAGGACAAGGTGGAGCACTGGTGGACAGAGGGGACAAC AGTGATGTCGACGTGATAGAGCTTCACGATTGCTTCTCTACCAATGAACTCCTGACTTAT GGCTATGATATGAGTAAAGAAGCTGCCAGGAAGTGCTATGAGAAGTCCGGCCTGGGTCCC CAGGAGATGGTGACTGACATGCCCACTACATTTGAAGAAAAAAGTGTTATTAAAATGGTT TCTAGTGAGGAGTTTGTGCAGAAGCATGGCCTGCAGTCCAAAGCTGTGGAAATTGTGGCA GATTTTCTGACTGTCTTACAATGCTGTCCCACCTCAGATGGTGCCGCAGCAGCAATTGTG TATTCCCAGTTCCAAGATGAATACAGCTTAGATGAGATAATGAAATCAAGGCCAGTTTTC AAGGTTGAACACTTTGCAAAAATTGGATGGAAAAATCATAAACACTCAGTTAATAACCCCG Conservative 57.9**%**; 78.5**%**; 0 Score 575.2; DB 10; Pred. No. 3.2e-133; 0; Mismatches 188; DB 10; Indels Length 19; 545 1026 665 1086 605 425 5 1146 485 906 846 365 786 305 245 999 185 125 546 966 726 909 6

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M62763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mori,T., Tsukamoto,T., Mori,H., Tashiro,Y. and Fujiki,Y. Molecular cloning and deduced amino acid sequence of nonspecific lipid transfer protein (sterol carrier protein 2) of rat liver: a higher molecular mass (60 kba) protein contains the primary sequence of nonspecific lipid transfer protein as its C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M62763.1 GI:202552
60 kDa protein; non-specific lipid
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAT60KDA 2599 bp mRAT 60 kDa protein and non-specific
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91239563
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GLGGAAVVTLYRMGFPBAASSFRTHQISAAPTSSAGDGFKANLIFKEIEKKLEEEGEE
FVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPDSDKKADCTITNADSDLLALM
                                                                                                                                                                                                                                                                                                MAQQLVQGGLANCVLALGFEKMEKGSLGTKYSDRSNPLEKHIDVLINKYGMSACPFAP
QLFGSAGKEHMETYGTKVEHFAKIGMKNHKHSVNNPYSQPCDEYSLDEINKSRPVFDP
LTVLQCCPTSDGAAAALVSSEEFVQKHGLOSKAVEIVAQEMVTDMPSTFEEKSVIKMV
GYDMSKEAARKCYEKSGLGPSDVDVIELHDCFSTNELLTYEALGLCPEGQGGALVDRG
                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/product="60 kDa protein"
/product="61 kDa protein id="AAA40622.1"
/protein id="AAA40622.1"
/db_xref="GI:20253"
/translation="MPSVALNSPRLRRVFVVGVGMTKFMKPGGENSRDYPDLAKEAGQ
/translation="MPSVALNSPRLRRVFVVGVGMTKFMKPGGENSRDYPDLAKEAGQ
/translation="MPSVALNSPRLRRVFVVGVGMTKFMKPGGENSRDYPDLAKEAGQ
/translation="MPSVALNSPRLRRVFVVGVGMTKFMKPGGENSRDYPDLAKEAGQ
                                                                                                                                                                 /note="larger precursor of non-specific lipid
carrier protein (sterol carrier protein 2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source text: Rattus norvegicus
                                                           translation="MGFPEAASSFRTHQISAAPTSSAGDGFKANLIFKEIEKKLEEEG/
EEFVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPDSDKKADCTITMADSDLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="clone TM-34"
46. .1689
                                                                                            /codon_start=1
/product="non-specific lipid transfer
/protein_id="AAA40623.1"
/db_xref="GI:202554"
                                                                                                                                                                                                                             TGKMNPQSAFFQGKLKIAGNMGLAMKLQSLQLQPDKAKL'
                                        LMTGKMNPQSAFFQGKLKIAGNMGLAMKLQSLQLQPDKAKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard_name="clone TM-34"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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     GAGCTGCTGTTGTCACCCTCTACAGAATGGG---TTTTCCCGAAGCTGCCAGCTCC-TTCA
                                      GAACTGTGGTTGTAACACTCTACAAGATGGGGTTTTCCCGGAAGCCGCCAGTTCCTTTTA
                                                                            GGAAA--GAGGCAGGTTCCTGGGGCAAAGGTGGCTCTGCAGCACAATTTAGGCCTTGGAG
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2382. .2387
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2580. .2585
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/note="mature non-specific lipid transfer carr:
(sterol carrier protein 2)"
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0; Mismatches 188;
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Sequence 842 from Paten
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AX306091.1 GI:17645404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Method for examining ischemic conditions
Patent: WO 0188188-A 842 22-NOV-2001;
School Juridical Person Nihon University
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                          Similarity 78.9
65; Conservative
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                           TGGTTGGCTTTGATATGAGTAAAGAAGCTGCAAGAAAATGCTATGAGAAATCTGGCCTGA
                                                                                  TGGCACAAGAAATGATGACTGATTTGCCAAGCTCGTTTGAAGAAAAAAGCATTATTAAAA
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
_455 c 576 g 53
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78.9%;
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Rodentia; Sciurognathi; Muridae;
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Pred. No. 9.1e-133;
0; Mismatches 186;
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AUTHORS
TITLE
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                                                                                                                                                                                                    non-specific lipid transfer protein; sterol carrier protein Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murif 1 (bases 1 to 2152)
Seedorf, U., Raabe, M. and Assmann, G.
Cloning, expression and sequences of mouse sterol-carrier protein-x-encoding cDNAs and a related pseudogene Gene 123 (2), 165-172 (1993)
                                                                                                                                                                                                                                                                                                                                              MUSSCP 2152 bp n
Mus musculus sterol-carrier protein
M91458
M91458.1 GI:293793
                                                                                                                                   Original source text: Mus musculus (library: 1-ZAP II) female adult, 6
Location/Qualifiers
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                                                   /organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6 x CBA"
/db xref="taxon:10090"
/sex="female"
/tissue_type="liver"
/dev stage="adult, 6-8 weeks"
/tissue_lib="1-ZAP II"
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                                                                                                        AAGCCGGAAAAGAGGCAAAGTTCCTGGTGCAAAGGTGGCTCTGCNGCATAATTTANGCAT
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2137. .2142
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/product="sterol-carrier protein
/protein_id="AAA40098.1"
/db_xref="GI:293794"
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78.9%;
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No. 9.1e-133;
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Rattus norvegicus (Norway
Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Characterization of a cDNA encoding DNA Cell Biol. 9 (3), 159-165 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Billheimer,J.T.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AAGAAGTTTTTGATTTTTGACTATCTTACAATGTTGTCCCACTTCAGATGGTGCTGCAG
                                                               TTAATAACCCGTATTCCCAGTTCCAAGATGAATACAGTTTAGATGAAGTGATGGCATCTA
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                                               TTAATAACCCGTATTCCCAGTTCCAAGATGAATACAGCTTAGATGAGATAATGAAATCAA
                                                                                                      GTTCGTGAAGAAATCGGTGGC----ATTTTTGCCTTCAAAGTGAAAGATGGCCCTGGA 1419
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milarity 77.8%;
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/protein_id="AAA42120.1"
/protein_id="AAA42120.1"
/db xref="id1:206872"
/db xref="id1:206872"
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translation="MVGYDMSKEAARKCYEKSGLISKGHPLGATGLAQCAELCWQLRGEA
LGLCPEGQGALVDRGDNTYGGKWVINPSGGLISKGHPLGATGLAQCAELCWQLRGEA
LGLCPEGQGALVDRGDNTYGGKWVINPSGGLISKGHPLGATGLAAPTSSAGDGFFKAN
LIFKEIEKKLEEEGEEFVKKIGGIFAFKVKDGPGGKEATWVDDVKNGKGSVLPDSDKK
ADCTITMADSDLLALMTGKMNPQSAFFQGKLKIAGNMGLAMKLQSLQLQPDKAKL"
300 g 332 t
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus'
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                               note="sterol carrier"
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                                                                                                                                                                                                                                                                                                                                                                                          'product="sterol carrier protein-2 mRNA"
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Pred. No. 6.1e-120;
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                                                                                                                                Homo sapiens (human)
Homo sapiens
Eukarvar
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat Mammalla; Eutheria; Primates; Catarrhini; Hominic 1 (bases 1 to 1500)

He,Z., Yamamoto,R., Furth,E.E., Schantz,L.J., Na; George,H., Billheimer,J.T. and Strauss,J.F. III. CDNAs encoding members of a family of proteins resterol carrier protein 2 and assignment of the gentromosome 1 p21---pter DNA Cell Biol. 10 (8), 559-569 (1991)
                                                                                                                                                                                                         Human sterol carrier M75884
                                                                                                                                                                                       M75884.1 GI:432976
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On Dec 6, 1993 this sequence version replaced gi:337996.
Original source text: Human liver cDNA to mRNA.
Location/Qualifiers
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                                                                 AAAGTGGGTCATAAATCCTAGTGGTGGACTGATTTCAAAGGGACACCCACTAGGCGCTAC
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/note="no polyA or polyA signal was found this cDNA clone, indicating that the mRNA partial at the 3' end"
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/product="sterol carrier protein-2"
/protein_id="AAA03558.1"
/protein_id="AAA03558.1"
/db_xref="GI:432977"
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82. .951
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/mol_type="mRNA"
/db_xref="taxon:9606"
/map="1p32"
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/clone_Tib="Clontech HL-1001b;HL-1115b"
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Original source text: Gallus 
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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sterol carrier protein-2.
Gallus gallus (chicken)
Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA--GGAGATTGAGAAGAAACTTGA----AGAGGAAGGGGAACAGTTTGTGAAGAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAGGNGGATTGAGAAGGAAACNTNAAAGAGGGAANGGGGAACAATTTGTGAAAGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTGAA---GCTGTTCCAACCAGCTCTGCAAGTGATGGATTTAAGGCAAATCTTGTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTGAAGCCNGTTCCAACCAAGCTCTGCAAGTNATNGGTTTAANGNAAAATCTNGTTTT
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KMVGYDMTKKAAAEKCFKKAGLKPTDUDVIELHDCFSVNEFITYEALGLCPEGKACDLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="White Leghorn"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     lib="lambda gt11"
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rary: lambda gtll) adult liver
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FVKKIGGVFAFKIKDGPGGKEATWVVDVKNGKGSVAVNSDKKADCTITMADTDLLALM
TGKMNPQTAFFQGKLKISGNWGMAMKLQNLQLQPGKAKL"
                  463 c
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                                                                                                                                           CTTGGTGCCACAGGCCTGGCGCAGTCGGCTGAACTCTGCTGGCAGCTGCGCGGCCTGGCC
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Listing first 45 summaries
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	B94757	14	σ		05.	37
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	G28960	10	ð	٧.	24.	34
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	10559	ø	ω	5	49.	31
	14816	14	(J)		55.	30
	B94802	14	4	5	56.	29
	B15888	14	52	٥.	58.	28
	F18063	10	7	9	62.	27
_	962	13	0		368.4	26
X433336 B)	X43333	13	N	7.	70.	25
84426 yq2:	8442	14	4	ω	86.	24
116787 ue:	11678	9	ω	0	0	23
551168 ALS	55116	9	w		6	22
12823 60	43282	10	4	<u>ب</u>	19.	21
B947142 AC	B94714	14	w	ω	30.	20
B153363 K	81533	<u>1</u> 4	N	4	9.	19
B162403 K-EST022	B16240	14	ø	Α.	4 3.	18
B316398 AGENCOUR	B31639	14	σ	რ	57.	17
E971366 60165153	E97136	10	52	7.	69.	16
M552173 A	M55217	12	S	7.	70.	15
694509 DKI	69450	9	7	9	95.	14
694422 DKI	69442	9	æ	0	۵ <u>1</u> .	13
25668 PT:	52566	9	-	۲	08.	12
B950754 A	9507	14	σ	۲	\vdash	11
951253 AGENCOUR	B95125	14	ū		μ	10
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G289834 60238473	G2898	10	92	7.	72.	7
K004860 Mus musc	K00486	片	7	ω.	76.	თ
293	C02933	11	96	œ	76.	տ

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JOURNAL COMMENT ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AU121360 LOCUS REFERENCE DEFINITION AUTHORS sequence. AU121360 AU121360.1 Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@bhi.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing:
Research Institute; cDNA library construction: Department Isogai,T.
HRI human cDNA project
Unpublished Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases: 1 to 817)
Communici v Tahii S. Saito.K. Kawai,Y., AU121360 HEMBB1 Homo sapiens cDNA clone HEMBB1002667 5', mRNA Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Homo sapiens (human) Yamamoto, J., Wakamatsu, A., GI:10936595 Nakamura, Y., Nagai, T., Sugano, S. and

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GTTTTAAAGGNGGATTGAGAAGGAAACNT
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/dev_stage="embryo, 10 weeks"
/clone_lib="HEWBB1"
/note="Vector: pME18SFL3"
l41 c 201 g 217 t
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/db_xref="taxon:9606"
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mol_type="mRNA"
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AGENCOURT 14007012 NIH MGC_186 Homo
IMAGE:30372857 5', mRNA sequence.
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plate: NDCM165 row: l column: 18
High quality sequence stop: 463.
Location/Qualifiers
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Tissue Procurement: Dr. Michael Brownstein and Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection
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1 (bases 1 to 828)
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ATTTTGGCCAGTGAAGCATTTGTACAGAAGTATGGCCTGCAATCCAAAGCTGTGGAAATT
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/clone lib="NHI MGC 186"
/clone lib="NIH MGC 186"
/note="Torgan: Pooled-Skin; Vector: pDNR-LIB; Site 1: SfiI
(ggccattatggc); Site 2: SfiI (ggccgctcggcc); Library is
oligo-dT primed and directionally cloned. cDNA was
prepared from a pooled samples of tissues from Skin,
meningss, duramatter, pia matter and choroid placuus. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGGCCGACCATTC-dT(30)BN-3'
Sequence: 5'-ATTCTAGAGGCCGGCCGGCCGACATTC-dT(30)BN-3'
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156 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.47 kb (range 0.50-4.0 kb) a 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
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'db_xref="taxon:9606"
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Plate:
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                                                                                                                                                                                 Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
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CB147601
CB147601.1 GI:28129068
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K-EST0203627 L11SNU35481
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1 (bases 1 to 609)

1 (bases 1, Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.
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                                                                                                                                                                                                                                                                                                                                                   Y.S.
                                                                                                 l: yongsung@mail.kribb.re.kr
e: 29 row: G column: 02
quality sequence stop: 609.
Location/Qualifiers

    Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

/organism="Homo Bapiens"
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/clone="L118NU354s1-29-G02"
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                           ACCAACGAACTCCTTACTTATGAAGCACTGGGACTCTGTCCAGAAGGACAAGGTGCAACG
                                                                                                     GAGAAATCTGGCCTGACACCAAATGATATTGACGTAATAGAACTTCACGATTGCTTTTCT
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                                                                                  GAGAAATCTGGCCTGACACCAAATGATATTGACGTAATAGAACTTCACGATTGCTTTTCT
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                                                                                                                                                                                         AAAAGCATTATTAAAATGGTTGGCTTTGATATGAGTAAAGAAGCTGCAAGAAAATGCTAT
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                                                                                                                                                                                                                                                                       AAAGCTGTGGAAATTTTTGGCACAAGAAATGATGACTGATTTGCCAAGCTCGTTTGAAGAA
                                                                                                                                                                                                                                                                                                                              GGTGCTGCAGCAGTTTTTGGCCAGTGAAGCATTTGTACAGAAGTATGGCCTGCAATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECORI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avoidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToploF' with electroporation method."
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/cell_tine="SNU-354"
/lab_host="Top10F/"
/clone_lib="LilsNU354s1"
/note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.1%;
99.8%;
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Pred. No. 1.1e-114;
0; Mismatches 1;
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Tissue Procurement: ATCC
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http://image.llnl.gov
plate: LLMM9723 row: j column: 15
High quality sequence stop: 598.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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ACTTCAGATGGTGCTGCAGCAGCAATTTTGGCCAGTGAAGCATTTGTACAGAAGTATGGC
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                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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181 ACTTCAGATGGTGCTGCAGCAGCAATTTTGGCCAGTGAAGCATTTGTACAGAAGTATGGC
                      Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 42 Row: m Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein This clone has the following problem: no 5' EST match.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                              Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: ang@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
Richards, S., Gibbs, R.A.
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CDNA Library Arrayed by: The I.M.A
DNA Sequencing by: Baylor College
Sequencing Center
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ATTTGTGAAAGAAAATNCGGNGGGAATTTTTGCCCTTCAAGGGGAAANAATGGCCCTGG
                                       GGCAAACCTCGTCTTTAA-
                                                                                                                                                         TGGAGGAACTGTGGTTGTAACACTCTACAAGATGGGGTTTTCCCCGGAAGCCCGCCAGTTCC
                                                                                                                                                                                                           AAGCCGGAAAAGAGCAAAGTTCCTGGTGCAAAGGTGGCTCTGCNGCATAATTTANGCAT
                                                                                                                                                                                                                                                             ACCCACTAGGCGCTACAGGTCTTGCTCAGTGTGCAGAACTCTGCTGGCAGCTGAGAGGGG
                                                                                                                                                                                                                                                                                               ACAACACTTACGGAGGAAAGTGGGTCATCAACCCTAGTGGAGGCCTCATCTCAAAGGGAC
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                                                               NGNAAAATCTNGTTTTAAAGGNGGATTGAGAAGGAAACNTNAAAGAGGGAANGGGGAACA
                                                                                         TTCAGGA--CGCACCAGGTTTCAGCTGCTCCCA--CCAGCTCTGCAGGGGATGGATTCAA
                                                                                                                  TTTTAGAACTCATCAAAATTGAAGCCNGTTCCAACCAAGCTCTGCAAGTNATNGGTTTAA
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/clone_Tib="NH MGC_12"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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Nature 409
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Mammalia; Eutheria;
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On Dec 6, 2002 this sequence version replaced gi:12836362.
Please visit our web site (http://genome.gsc.riken.go.jp/) for
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Analysis of the mouse transcriptome based on of 60,770 full-length CDNAs
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/strain="C5/BL/6J"
/db_xref="FANTOM_DB:1300002N20"
/db_xref="MGI:1855024"
/db_xref="taxon:10090"
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/db_xref="MGI:98254"
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/clone_Tib="RIKEN full-length enriched
/dev_stage="adult"
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/db xref="taxon:9606"
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/tlssue_type="transitional cell papilloma, cell line"
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://imagg.llnl.gov
Plate: LLAM10161 row: d column: 21
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence start: 5
High quality sequence stop: 586
Location/Qualifiers
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Tissue Procurement: ATCC
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Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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GAAATGATGACTGATTTGCCAAGCTCGTTTGAAGAAAAAAGCATTATTAAAATGGTTGGC
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/clone_lib="NIH_MGC_84"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC_Library."
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Fax: 86-
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Chinese National Human
351 Guo Shoujing Road,
201203, P. R. China
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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                                                                                                                                                                       l: hanzg@chgc.sh.cn
clone is available at CHGC
Location/Qualifiers
                                                                                                                                                                                                                      86-21-50801919 (ex.45)
86-21-50801922
   /clone_lib="GLC"
/note="Vector: pBluescript
XhoI"
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                                               /tissue_type="corresponding
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLCDJE04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:9874317
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CB951253.1
EST.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein Labora
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                         1 (bases 1 to 757)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                 CB951253 757 bp
AGENCOURT 13445466 NIH MGC 177 Mus
IMAGE:30316161 5', mRNA sequence.
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                                                                                                                                                       Mus musculus
Eukaryota; Metazoa;
                                                              Contact: Robert Strausberg, Ph.D.
                                                                               Unpublished
                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                      Mus musculus (house
                                                                                                                                                                                                                                                                                                                                                              TGATGGATTTAAGGCAAATCTTGTTTTTAA--GGAGATTGAGAAGAAAACTGAAGA 646
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Rodentia;
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Sciurognathi; Muridae;
                                                                                               Mammalian
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Laboratory

Collection

Euteleostomi;

29-APR-2003

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648 360 588 300 468 180 408 120 348

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Murinae;

Mus.

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GCTGAGAGGGGAAGCCGGAAAAGAGGCAAAGTTCCTGGTGCAAAGGTGGCTCTGCNGCAT
                                                                              CTCAAAGGGACACCCACTGGGCGCAACAGGTCTGGCTCAGTGCGCGGAGCTCTGCTGGCA
                                                                                                                                                                                 GGACAGAGGGGACAACACTTACGGAGGAAAGTGGGTCATCAACCCTAGTGGAGGCCTCAT
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//lab host="DH10B (T1-phage-resistant)"
//clone_lib="NIH MGC_177"
//clone_lib="NIH MGC_177"
//clone_lib="NIH MGC_177"
//clone_lib="NIH MGC_177"
//clone_lib="NIH MGC_177"
//clone_lib="NIH MGC_177"
//cloned. 5' and sirectionally cloned. 5' and 3'
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-ARCCAGTGGTATCAACGCAGAACTGGCCATTACGGCCGG-3' and
5'-ARTCTAGAAGGCCGACAACTGGCCATTACGGCCGG-3' and
5'-ATTCTAGAGGCCGAGGCCGACATTGGCCATTACGGCCGG-3' and
5'-ATTCTAGAGGCCGAGGCCGACATTGGCCCGG-3' and
6'-ATTCTAGAGGCCGAGGCGCGACATTGGGCCGG-3' and
5'-ATTCTAGAGGCCGAGCGGCGG-1' clonech
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIHH, NIH). Note: this is a NIH MGC Library."
12 a 174 c 210 g 160 t 1 others
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/mol_type="mRNA"
/db_xref="taxon:10090"
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Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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NIH-MGC http://mgc.nci.nih.gov/.
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//ab host="DH10B (T1-phage-resistant)"
/lab host="DH10B (T1-phage-resistant)"
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                                                       Leroy Hood
University of Washington
Department of Molecular Biotechnology,
Washington, Seattle, WA 98195
Tel: 5106280100
Fax: 5106280108
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 914)
Huang, G.M., Ng, W.l., Farkas, J., He, L., Liang, H.A., Gand Hood, L.
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Matches 581; Conserv
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DKFZp313F1641 rl 313 (synonym: h
DKFZp313F1641-5', mRNA sequence.
AL694422

AL694422.1 GI:19617879
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  Eukaryota; Metazoa; Chordata;
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GGGGTGGTGGGAT
                                                 GGNATTTTNNCCCTCCAAAGGNGGAAAGATGGCCCCTGGGGGGAAAAAAGGCCNCCCT
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/clone lib="tumor1"
/note="Organ: Prostate; Vector: pBluescript; Directional
/note="Torgan: Prostate; Vector: pBluescript; Directional
cDNA library was constructed using Lambda ZP II kit
(Stratagene). mRNA was extracted from a frozen prostate
tumor tissue (Mayo Clinics)."

a 174 c 255 g 189 t 38 others
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Pred. No. 2.1e-94;
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sequence

Craniata;

Vertebrata;

Euteleostomi;

583 bp mRNA lonym: hlcc2) Homo

sapiens linear

EST

21-MAR-2002 clone

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REFERENCE
AUTHORS
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This clone (DKFZp313F1641) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKPZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 583)

Koehrer, K., Beyer, A., Mewes, W., Weil, B. and Wiemann, S.

EST (Koehrer, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.)

Unpublished
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                GATAATACATATGGAGGAAAGTG 583
                                           GATAATACATATGGAGGAAAGTG 562
                                                                          ACTTATGAAGCACTGGGACTCTGTCCAGAAGGACAAGGTGCAATGCTGGTTGATAGAGGA
                                                                                          ACTTATGAAGCACTGGGACTCTGTCCAGAAGGACAAGGTGCAACGCTGGTTGATAGAGGA
                                                                                                                                ACACCAAATGATATTGACGTAATAGAACTTCACGATTGCTT
                                                                                                                                                  ACACCAAATGATATTGACGTAATAGAACTTCACGATTGCTTTTCTACCAACGAACTCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="DKRZp313F1641"
//dev_stage="adult"
//lab_host="DH10B"
/clone=lib="313 (synonym: hlcc2)"
/note="Vector: pTriplEx2; Site_1: SfiIA;
cDNA-collection"
97 c 121 g 166 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 7.1e-93;
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Query Match
Best Local Similarity
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This clone (DKFzp313G1541) is available at the RZPD i Please contact the RZPD: Ressourcenzentrum, Heubnerwe Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 577)

Koehrer,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.
EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACCCGTATTCCCCAGTTCCAAGATGAATACAGTTTAGATGAAGTGATGGTCTAAAGAA
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                                                                                                                  ATGGTTGGCTTTGATATGAGTAAAGAAGCTGCAAGAAAATGCTATGAGAAATCTTGGCCTG
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cDNA-collection"
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Pred. No. 1.2e-91;
0; Mismatches 1
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Qy Db	540 GATAATACATATGGAGG 556
RESULT 15 BM552173 LOCUS DEFINITION	BM552173 AGENCOURT
ACCESSION VERSION KEYWORDS SOURCE	BM552 BM552 BM552 EST.
ORGANISM	-3-
REFERENCE AUTHORS TITLE	1 (bases 1 to 1051 NIH-MGC http://mgc. National Institutes
COMMENT	Ontact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM12260 row: e column: 02 High gmality sequence ston: 653.
FEATURES sourc	ro
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BASE COUNT	318
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당 상	1 CTCACCCAGTTGCTCCTCAGATGTTTGGGTATGCTGGAAAAGAACATATGGAAAAAATATG 60
Q	61 GAACAAAAATTGAACACTTTGCAAAAAATTGGATGGAAAAAATCATAAACATTCAGTTAATA 120
Dъ	367 GAACAAAAATTGAACACTTTGCAAAAATTGGATGGAAAAATCATAAACATTCAGTTAATA 426
\$ 8	121 ACCCGTATTCCCAGTTCCAAGATGAATACAGTTTTAGATGAAGTGATGGCATCTTAAAGAAG 180
B 64	181 TTTTTGATTTTTTGACTATCTTACAATGTTGTCCCACTTCAGATGGTGCTGCAGCAGCAA 240 .

B &	dd VQ	d dq	Db Qy	Qy db
480 AC 787 AC	421 CA 727 CA	361 TG 667 TG	301 TG 607 TG	241 TT 547 TT
ACTTATGAAGCACTGGGACTCTGTCCAGAAGGACAAGG 517	CACCAAATGATATTGACGTAATAGAACTTCACGATTGCTTTTCTACCAACGAACT-CCTT	TGGTTGGCTTTGATATGAGTAAAGAAGCTGCAAGAAAATGCTATGAGAAAATCTGGCCTGA 420	TGGCACAAGAAATGATGACTGATTTGCCAAGCTCGTTTGAAGAAAAAAGCATTATTAAAA 360 	TTTTGGCCAGTGAAGCATTTGTACAGAAGTATGGCCTGCAATCCAAAGCTGTGGAAATTT
	479 786	726	360 666	300

Search completed: November 27, 2003, 12:28:18 Job time : 2685.01 secs

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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seq length: 2000000000
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SUMMARIES

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į	S S S	266	322.8	573.4	769	769	769	978	Score
	S	26.8	32.5	57.7	77.4	77.4	77.4	98.4	Query Match Length DB
	1217	1837	432	2152	3053	3053	2663	994	Length 1
į	ž	23	25	24	23	23	22	20	
	ABI.1 AAA1	ABL16479	ABX40513	ABI99762	ABV27671	ABV21847	AAH57501	AAX40096	ID
	Drogonhila melanog	Drosophila melanog	Bovine EST associa	Mouse ischaemic co	Human prostate exp	Human prostate exp	Human liver cell s	Gastric cancer ass	Description

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Drosophila melanog Staphylococcus aur Staphylococcus aur Chemically treated Human immune syste Chemically treated Gemically treated S. cerevisiae esse Methanococcus jann	Human DNA tor a no Tumour suppressor DNA transcription Human prostate exp Drosophila melanog Drosophila melanog	Human prostate exp Human prostate exp Pyrococcus abyes! Phase-1 Rat CT gen Human prostate exp Malaria-specific D DNA encoding argin Staphylococcus aur Mycoplasma genital	Mycobacterium tube Mycobacterium tube Bovine EST associa Human secreted pro Human genome fragm Human GDP-mannose Methanococcus jann	H

ALIGNMENTS

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RESULT 1

AAX40096

ID AAX40096 standard; DNA; 994 BP.

XX

AC AAX40096;

XX

DT 02-JUL-1999 (first entry)

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DT 02-JUL-1999 (first entry)

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Cancer associated antigen; diagnosis; research; treatment; human;

XX

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Cancer associated antigen; diagnosis; research; treatment; human;

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W prostate cancer; colon cancer; gastric cancer; renal cancer; lung cancer;

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PN wO9904265-A2.

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PN wO9904265-A2.

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PP 15-JUL-1998; 98WO-US14679.

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PF 12-JUL-1997; 97US-0896164.

PR 17-JUL-1997; 97US-0861599.

PR 10-CCT-1997; 97US-0961765.

PR 10-CCT-1997; 97US-0961765.

PR 11-CCT-1997; 97US-0961765.
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Query Match
Best Local S
Matches 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and lung cancer
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                          ATAATACATATGGAGGAAAGTGGGTCATAAATCCTAGTGGTGGACTGATTTCAAAGGGAC
                                                                                                             CTTATGAAGCACTGGGACTCTGTCCAGAAGGACAAGGTGCAACGCTGGTTGATAGAGGAG
                                                                                                                                                                                               CACCAAATGATATTGACGTAATAGAACTTCACGATTGCTTTTCTACCAACGAACTCCTTA
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  ATAATACATATGGAGGAAAGTGGGTCATAAATCCTAGTGGTGGACTGATTTCAAAGGGAC
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AAH57161 to AAH57576 represent cell and tissue specific polynucleotide sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tissue specific; diagnosis; prair, process; so, lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; so; metabolic disease; developmental disease; cytostatic; immunomodulatory; neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
                                                                                                                                                                                                                                                                               New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTATGAAGCACTGGGACTCTGTCCAGAAGGACAAGGTGCAACGCTGGTTGATAGAGGAG
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  NGNAAAATCTNGTTTTAAAGGNGGATTGAGAAGGAAACNTNAAAGAGGGAANGGGGAACA
                                                                                                                      TGGAGGAGCTGTGGTTGTAACACTCTACAAGATGGG--TTTTTCCGGAAGCCGCCAGTT-C
                                                                                                                                          TGGAGGAACTGTGGTTGTAACACTCTACAAGATGGGGTTTTTCCCGGGAAGCCGCCAGTTCC
                                                                                                                                                                                                                        AAGCCGGAAAAGAGGCAAAGTTCCTGGTGCAAAAGGTGGCTCTGCNGCATAATTTANGCAT
                                                                                                                                                                                                                                                                           ACCCACTAGGCGCTACAGGTCTTGCTCAGTGTGCAGAACTCTGCTGGCAGCTGAGAGGGG
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                                      TTTTAGAACTCATCAAATTGAA---GCTGTTCCAACCAGCTCTGCAAGTGATGGATTTAA
                                                                                                                                                                                               AAGCCGGAAA--GAGGCAAGTTCCTGGTGCAAAGGTGGCTCTGCAGCATAATTTAGGCAT
                                                                                                                                                                                                                                                                                                                 ACCCACTAGGCGCTACAGGTCTTGCTCAGTGTGCAGAACTCTGCTGGCAGCTGAGAGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.4%;
91.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Query Match Best Local S Matches 899

Local Similarity nes 899; Conserv

77.4%; ilarity 91.3%; Conservative

Score 769; DB 23; Pred. No. 9.6e-207; 0; Mismatches 66;

20;

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887

other; Length 3053; Indels

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the CC specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) cancer in a patient;
(d) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) assessing the prostate cell carcinogenic potential of a compound;
(f) assessing the prostate cell carcinogenic potential of a compound;
(c) determining whether prostate cancer has metastasized in a patient;
(d) assessing the aggressiveness or inaliance.
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate pharmacogenomic
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                       is also useful as a pharmacodyanamic or pharmacogenomic
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                                                                                                                                                                                                                                                isolated nucleic acid molecule associated with cancerous state ate cells and correlating with presence of prostate cancer, usef etecting presence of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prostate expression marker cDNA 21838.
                                                                                                                                                                                                                                                                                                                                                     MILLENNIUM
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2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-2119007P.
2000US-255281P.
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gene; ss.
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                           marker
                                                                                                                                                                                     ) comprising of the
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RESULT 4
ABV27671
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                                                                                                                                                                                                                     GGCAAATCTTGTTTTAA--GGAGATTGAGAAGAAACTTGA----AGAGGAAGGGGAACA
                                                                                                                                                                                                                                                                              GGGGTAAAAGANGGCCACCCTGGGG
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                                                                                     GGGTAAAGAGGCCACCTGGGTGGTG
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Matches
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(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compound;

(g) determining whether prostate cancer has metastasized in a patient;

(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, use for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 5667; 11750pp; English.
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                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                   GAACAAAATTGAACACTTTGCAAAAATTGGATGGAAAAATCATAAACATTCAGTTAATA
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                                                                                   ACCCGTATTCCCAGTTCCAAGATGAATACAGTTTAGATGAAGTGATGGCATCTAAAGAAG
                                                                                                                     GAACAAAATTGAACACTTTGCAAAAATTGGATGGAAAAATCATAAACATTCAGTTAATA
                                                                                                                                                                                      CTCACCCAGTTGCTCCAGATGTTTGGGTATGCTGGAAAAGAACATATGGAAAAATATG
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; 2000US-189862P.
; 2000US-207454P.
; 2000US-211314P.
; 2000US-219007P.
; 2000US-255281P.
                                                                                                                                                                                                                                                      Conservative
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91.3%;
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                                                                                                                                                                                                                                                                      Score 769; DB 23; Pred. No. 9.6e-207;
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181

TTTTTGATTTTTTGACTATCTTACAATGTTGTCCCACTTCAGATGGTGCTGCAGCAGCAA

180

240 767 120

647 60

707

20;

Gaps

in a patient;

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RESULT 5
AB199762
ID AB19
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                                                                                                                                                         vasospastic ischaemia;
                                                                                                                                                                                    Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
                                                                                                                                                                                                                                   Mouse ischaemic condition related cDNA sequence SEQ ID NO:842
                                                                                                                                                                                                                                                                                         07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                            ABI99762 standard; cDNA; 2152
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                                                                                                                                                         ischaemic condition; ischaemic disease;
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The present invention describes a method for examining ischaemic cc conditions, comprising measuring the expression levels of particular cc genes (I) in a test sample or determining the expression profile of a cc gene group in the sample comprising genes selected from (I). The method cc is useful for examining the ischaemic condition (e.g. compressive cc ischaemia, occlusive ischaemia or vasospatic ischaemia) by measuring cc expression levels of particular genes (AB199202 to AB19912, encoding cc expression profile of a gene group comprising these genes. The cc expression profile of a gene group comprising these genes. The cc expression levels or expression profiles produced by these genes are cc used as an indicator when screening for ischaemic condition-improving cc drugs or therapeutics for ischaemic diseases. AB19913 and AB199914 cr represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 2087-2091; 2690pp; English
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Query Match Best Local Similarity Sequence 2152 BP; 586 A; 455 C; 576 G; 535 T; 0 other; 57.7%; 78.9%; Score 573.4; DB 24; Lengtl Pred. No. 1.6e-151; 0; Mismatches 186; Indels Length

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DNA; 1837

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CC Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-cc translated sequence that functions in the cell to cause termination of CC transcription and addition of polyademylated ribonucleotides to a 3' end CC of the mRNA molecule; and (2) determining a level or pattern of a 3' end CC molecule in a bovine cell or tissue comprising: (a) incubating a marker CC nucleic acid (comprising any of the 15112 nucleic acid sequences or its CC complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the CC detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is predictive of the level or pattern of the complementary nucleic acid is used for determining a level or pattern of the mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically constructs for use in cattle gene expression, or for genetically constructs for use in cattle gene expression, or for genetically constructs for use in cattle gene expression, or for genetically constructs for use in cattle gene expression, or for genetically constructs for use in cattle gene expression, or for genetically constructs for use in cattle gene expression, or for genetically constructs for use in cattle gene expression, or for genetically constructs for use in cattle gene expression of the 15112 bovine constructs for use in cattle gene expression of the specification but was obtained in electronic format from the USBTO web site:

CC sequata uspto.gov/sequence.html?DocID=20020137139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 432 BP; 127 A; 75 C; 122 G; 108 T; 0 other;
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GCATCGGAGGAGCTGTCGTTGTTACGCTGTACAAGATGGGCTTTCC
                                          GCATTGGAGGAACTGTGGTTGTAACACTCTACAAGATGGGGTTTTTC
                                                                                              GGGGAAGCCGGAAA--AAGGCAAGTTCCTGGTGCAAAGGTTGCTCTGCAGCATAATATAG
                                                                                                                       GGGGAAGCCGGAAAAGAGGCAAAGTTCCTGGTGCAAAGGTGGCTCTGCNGCATAATTTAN
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Pred. No. 5.1e-81;
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1837
                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form specification, but was obtained in electronic fat ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid genes from Drosophila and
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11-JUL-2000; 2000US-0614150
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                                     TTGTAGGCATGGAGATGGCCAGTGACCCGGCGTCCACCTTTGCCGACAAGAGCTTGATGA
                                                            TTTTGGCACAAGAAATGATGACTGATTTGCCAAGCTCGTTTGAAGAAAAAAGCATTATTA
                                                                                      CCATTCTCGCCTCCGAGGCCTTCGTGCGTCGCCACGGATTGGAAAAGCAGGCTGTCGAAA
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                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                       sequences (ABL01840
(ABB57737-ABB72072)
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New isolated nucleic a genes from Drosophila interactions -
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SEQ ID NO 1456; 21pp + Sequence Listing; English
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                                                                                                                                             ABX42390 standard; cDNA; 346 BP
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                                                                                                                                                                                                                          TGGTGCTGTTGTGCCTTGTATCGTCTGGGTTT 1147
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Pred. No. 4.6e
0; Mismatches
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1.6e-63;
1es 292;
mapping; gene identification;
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                                                                                                                                                                                                                  Query Match
Best Local Sim
Matches 289;
                                                                                                                                                                                                                                                                                                       Sequence 346 BP; 96 A; 66 C; 99 G; 85 T; 0 other;
                                                                                                                                                                                                                                                                                                                                          was obtained in electronic format from the USPTO we seqdata.uspto.gov/sequence.html?DocID=20020137139..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid associated with lactation, and muscle and deposition, useful for genome mapping, gene identification analysis, cattle breeding, or for genetically improving cat
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11-JAN-2000;
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                                                                        ATGGAGGAAAGTGGGTCATAAATCCTAGTGGTGGACTGATTTCAAAGGGACACCCACTAG
                                                                                                                                   SEQ'ID No 7555; 245pp; English
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                                                                                                                                                                                                                  Score 253; DB 25;
Pred. No. 2.5e-61;
D; Mismatches 42
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134

ATGGAGGAAAGTGGGTCATAAATCCTAGTGGCGGATTAATTTCAAAGGGGCACCCACTTG

193 609 133 549

489 73

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ABSJULT 10
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The invention relates to a purified nucleic acid molecule associated with CC lactation or muscle and fat deposition (designated LMFD), derived CC from cattle, and the LMFD nucleic acid can specifically hybridise to a Second nucleic acid molecule comprising any of 15112 nucleotide CC sequences, appearing as ABX34836-ABX49947, or complements of them. CC Also included are; (1) a transformed cell having a nucleic acid CC comprising an LMFD nucleic acid linked to a promoter and a 3' non-CC translated sequence that functions in the cell to cause termination of CC transcription and addition of polyadenylated thouncleotides to a 3' end CC molecule in a bovine cell or tissue comprising: (a) incubating a marker CC nucleic acid (comprising any of the 1512 nucleic acid sequences or its CC complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the CC detection of the molecule; and (b) detection of the complementary nucleic acid permits the CC complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern
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(MATH/)
(TAON/)
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11-JAN-2000;
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                         Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in th genome corresponding to positions where M. tuberculosis strains CDC
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                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                        New isolated nucleic a genes from Drosophila interactions -
                                                                                                                 Claim 1; SEQ ID NO 8077; 21pp + Sequence Listing; English
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GTGGTGCTGTTGTGCCTTGTATCGTCTGGGTTT
                           GAGGAACTGTGGTTGTAACACTCTACAAGATGGGGTT
                                                                                      gccggaaaaggaggcaaagtrccrggrgcaaaggrggcrcrgcngcaraarrrangcarrg
                                                                                                                      CCTCTGGGCGCCACGGGTCTGGCACAATGTGCTGAGCTCTGCTGGCAGCTCCGTGGATTG
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Pred. No. 4.3e-49;
0; Mismatches 248;
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RESULT 14
ABL26826/c
Drosophila
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                                                                                                  ABL26826
             WO200171042-A2
                          Drosophila melanogaster
                                             Drosophila; developmental
                                                                                      ABL26826;
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                                                          melanogaster genomic polynucleotide
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                                             biology; cell signalling;
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GCCGGAAAAGAGGCAAAGTTCCTGGTGCAAAGGTGGCTCTGCNGCATAATTTANGCATTG
                                                     CCTCTGGGCGCCACGGGTCTGGCACAATGTGCTGAGCTCTGCTGGCAGCTCCGTGGATTG 3414
                                                                                    CCACTAGGCGCTACAGGTCTTGCTCAGTGTGCAGAACTCTGCTGGCAGCTGAGAGGGGAA
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0; Mismatches 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
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(ABB57737-ABB72072)
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ALIGNMENTS

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RESULT 1

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Sequence 21, Application US/09835992A

Patent No. US20020037541A1

Patent No. US20020037541A1

PATENTIAL INFORMATION:

APPLICANT: Obsta, Yuichi

TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING GASTRIC CANCER AND TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING GASTRIC CANCER AND TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING GASTRIC CANCER

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                                CTTATGAAGCACTGGGACTCTGTCCAGAAGGACAAGGTGCAACGCTGGTTGATAGAGGAG
                                                                                        CACCAAATGATATTGACGTAATAGAACTTCACGATTGCTTTTCTACCAACGAACTCCTTA
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Pred. No. 2.9e-248;
0; Mismatches 0;
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US-09-960-352-5678
; Sequence 5678, Application
; Patent No. US20020137139A1
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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUCLEIC AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT FILING APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5678
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 360; Conserv
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                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Bos taurus
ORGANISM: TAPORMATION: Clone
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                  GGAGATAATACATATGGAGGAAAGTGGGTCATAAATCCTAGTGGTGGACTGATTTCCAAAG
                                                                              CTTACTTATGAAGCACTGGGACTCTGTCCAGAAGGACAAGGTGCAACGCTGGTTGATAGA
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milarity 88.7%;
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUCLEIC ACID AND EAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

INUMBER OF SEQ ID NOS: 15112

SEQ ID NO 7555

LENGTH: 346

TYPE: DNA

OTHER INFORMATION: Clone ID: 32-LIB34-076-Q1-E1-H7

US-09-960-352-7555
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US-09-960-352-7555
; Sequence 7555, Application
; Patent No. US20020137139A1
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Sequence 647, Application US/09960352
PATENT NO. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Wastren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION /
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 647
LENGTH: 314
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 03-LIB34-050-Q1-E1-A11
US-09-960-352-647
                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-10-156-761-5843
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APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
US-10-156-761-5843
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Best Local Similarity
Matches 273; Conserv
                                                                                                                                                                                                                                                                                                                                           Sequence 5843, Application US/10156761 Publication No. US20030119018A1
               NAME/KEY: CDS
LOCATION: (1)
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Pred. No. 9.1e-53;
0; Mismatches 40;
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Query Match

19

Score 196.2;

80

14;

Length 1236;

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RESULT 6
US-10-156-761-1
(Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
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                                                                                APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE, OF INVENTION: NOVEL FOLYNUCLEOTIDES
FILE REFERENCE: 249-262
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Matches
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
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0; Mismatches 325;
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; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t
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LENGTH: 90
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Best Local Similarity 55.1%;
Matches 402; Conservative
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PRIOR APPLICATION NUMBER: JP:
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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                                                            CCAGGTCCCGGGCGCCCGGGTGGGTCTCGCGCACAACATCGGACTGGGCGGAGCGGCGGT
                                                                                          CAAAGTTCCTGGTGCAAAGGTGGCTCTGCNGCATAATTTANGCATTGGAGGAACTGTGGT
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Pred. No. 3e-39
0; Mismatches
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RESULT 7 US-09-960-352-2946

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; SEQ ID NO 8890
; LENGTH: 249
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone II
US-09-878-574-8890
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US-09-878-574-8890
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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 2946
LENGTH: 412
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 13-LIB34-005-Q1-E1-D1
US-CONSTRUCTED OF SEC OF SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8890, Application US/09878574 Patent No. US20020110548A1
                                                                                Query Match
Best Local Similarity
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                                                           Matches 159;
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                                                                                                                                                                                                                                                                                                                                      APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)8
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
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Local Similarity 86.0%;
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                                                        Conservative
                                                                                9.3%;
                                                                                                                                                                                                     ID: 701101811H1
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Pred. No. 5.9e-40;
                                                                                Score 92; DB 10;
Pred. No. 3.4e-14;
                                                           Mismatches
                                                                                                              Length 249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Gaiger, Alexander

APPLICANT: Gordon, Brian

APPLICANT: Gordon, Brian

APPLICANT: Gordon, Brian

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER

FILE REFERENCE: 210121.572

CURRENT FILING DATE: 2002-03-19

NUMBER OF SEQ ID NOS: 1863

SOFTWARE: FASTESEQ for Windows Version 4.0

SEQ ID NO 364

LENGTH: 553

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: 539

OTHER INFORMATION: n = A,T,C or G
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US-10-102-524-364
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  RESULT 10
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Best Local Similarity
Matches 205; Conserv
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Publication No. US20030109434A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238
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                                                                                                                                                                                                                                                           881 NAAAGAGGGAANGGGGAACAATTTGTGAAAGAAAATNCGGNGGGAATTTTTGCCCCTTCA 940
                                                                                                                                                                                                                                                                                                                                                                             821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         761 TCCCGGAAGCCGCCAGTTCCTTTTAGAACTCAAAATTGAAGCCNGTTCCAACCAAGC 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  701 CTGCNGCATAATTTANGCATTGGAGGAACTGTGGTTGTAACACTCTACAAGATGGGGTTT 760
                                                                                                                                                                                                                                                                                                                                                                                                                                     59
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                                                                                                                                                                                                                                                                                                                                                        TCTGCAAGTNATNGGTTTAANGNAAAATCTNGTTTTAAAGGNGGATTGAGAAGGAAACNT 880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCTATCTTGTGCAGAGTTTGTTGTTGTAAACACAATTTGCCATCACAAGCTGTTG
                                                                                                                                            AGGGGAAANAATGGCCCTGGGGGGTAAAAGANGGCCACCCTGGGG 985
                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCGGAAGCCGCCAGTT-CTTTTAGAACTCATCAAATTGAA---GCTGTTCCAACCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCAGCATAATTTAGGCATTGGAGGAGCTGTGGTTGTAACACTCTACAAGATGGG--TT
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                                                                                      AGGTGAAAG-ATGGCCCTGGGGGTAAAGAGGCCACCTGGGTGGTG
                                                                                                                                                                                                        A----AGAGGAAGGGAACAGTTTGTGAAGAAAATCGGTGGT-----ATTTTTTGCCTTCA
                                                                                                                                                                                                                                                                                                                    TCTGCAAGTGATGGATTTAAGGCAAATCTTGTTTTTAA--GGAGATTGAGAAAAACTTG 172
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71.9%;
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Pred. No. 2.5e-13;
0; Mismatches 62;
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US-10-027-632-34139/c
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; OTHER INFORMATION: n = A,T,C
US-10-027-632-34138
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,368
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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                                            PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34139, Application US/10027632 Publication No. US20030204075A9
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Best Local !
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                                                                                                                                                                                                                                                                            FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                          APPLICATION NUMBER: US 60/185,218
FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 GTATGGCCTGCAATCCAAAGCTGTGGAAAT 298
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Pred. No. 2.
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SOFTWARE: FastSEQ for Windows V

SEQ ID NO 34138

; LENGTH: 938

; TYPE: DNA

; ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 34139
                                                                                                                                                         Matches
                                                                                                                                                                                                  Query Match
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ORCANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(938)
OTHER INFORMATION: n = A,T,C o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 108827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(938)
OTHER INFORMATION: n = A,T,C
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Similarity 83.3%;
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Similarity 83.3%;
                                    GTATGGCCTGCAATCCAAAGCTGTGGAAAT 298
                                                                                                                     TTGTCCCACTTCAGATGGTGCTGCAGCAGCAATTTTGGCCAGTGAAGCATTTGTACAGAA 268
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                                                                                                                                                                              Score 67.2; DB 13; Pred. No. 2.5e-07;
                                                                                                                                                             Mismatches
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/16,358
PRIOR APPLICATION NUMBER: US 60/16,358
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/166,002
PRIOR PRIOR PRIOR DATE: 1999-09-28
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR TILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PRILING DATE: 2000-03-29
PRIOR PRILING DATE: 2000-03-29
PRIOR PRILING DATE: 2000-03-29
PRIOR PRILING DATE: 2000-03-24
PRIOR PRILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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Best Local Similarity
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CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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SOFTWARE: FastSEQ for Windows Version 4.0
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NAME/KEY: misc_feature
LOCATION: (1)...(938)
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ENGTH: 938
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Pred. No. 2
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; ORGANISM: Human
US-10-027-632-103694
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 103694
LENGTH: 2432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 103695, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                        SEQ ID NO 103695
                                                                                                                        Query Match
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                                                                                  Matches
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.1.29

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 1999-09-28
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Local Similarity 51.9%;
es 96; Conservation
                                                                                                         Local
                             305 ACAAGAAATGATGACTGATTTGCCAAGCTCGTTTGAAGAAAAAAGCATTATTAAAATGGT 364
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                                                                                                         Similarity
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Pred. No. 1.4;
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Minimum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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3 US-09-103-840A-2
3 US-09-103-840A-2
3 US-08-916-421B-1
4 US-08-916-421B-1
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RESULT 1 US-08-895-164-21 Sequence 21, A Patent No. 661 Patent No.	
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RESULT 2
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
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LENGTH: 4411529
TYPE: DNA
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Best Local Similarity 57.1%;
Matches 428; Conservative
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TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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RESULT 3 US-09-103-840A-2/c

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Best Local Similarity
Matches 426; Conserv
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OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the OTHER INFORMATION: represent a, t, c or g
-09-103-840A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DNA SEQUENCES FOR STRA.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
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 GGAAAAGAGGCAAAGTTCCTGGTGCAAAGGTGGCTCTGCNGCATAATTTANGCATTGGAG
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RESULT 4
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SOFTWARE: PatentIn vers
SEQ ID NO 1
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TITLE OF INVENTION:
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APPLICANT: Bult et al.
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NAME/KEY: misc feature
LOCATION: (163385) (163385)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (191989) (191989)
OTHER INFORMATION: n equals a, t
                                                                                                     NAME/KEY: misc_feature
LOCATION: (98266).. (98266)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
LOCATION: (98343).. (98343)..
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
LOCATION: (10398).. (10398)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
LOCATION: (10398).. (1048948)..
LOCATION: (148948).. (148948)
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PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
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NAME/KEY: misc feature
LOCATION: (28222)...(28222)
OTHER INFORMATION: n equals
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LOCATION: (98159)..(98159)
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LOCATION: (84773)..(84773)
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NAME/KEY: misc feature
LOCATION: (319226)...(319226)

OTHER INFORMATION: n equals

OTHER INFORMATION: n equals
                          NAME/KEY: misc feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals
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LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a,
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LOCATION: (674435)..(674435)
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LOCATION: (559167)...(559167)
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LOCATION: (312837)...(312837)
OTHER INFORMATION: n equals a,
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LOCATION: (234220)..(234220)
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NAME/KEY: misc_feature
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LOCATION: (5592
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US-08-916-421B-1
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                                                                  LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a,
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LOCATION: (1569020)..(156902
OTHER_INFORMATION: n equals
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LOCATION: (1349491)...
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OTHER INFORMATION: n equals
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밁 맑 밁 Ś S á á S 밁 В Ş Matches 307; Query Match Best Local 1610396 1610105 1610216 1610276 1610336 Local 406 346 226 106 9.3%; Similarity 49.4%; ATATCATCTÁCATCAAAGCAAGTGTTCAAGCATCAGATA-----TCAACTCCTCACCAGTTGCTGAGCCTTTAAGATTACTACATTGCTCACCAGTTTCAGATG ÀÀAÀACGCCTCAÀAAAATAGATATGCACAATTCCCATTTAAGGTTACATTGGAGCAGGTTC 1610337 AACATTCAGTTAATAACCCGTATTCCCAGTTCCAAGATGAATACAGTTTAGATGAAGTGA 165 **ANATGGCANATATAGANCCANAGGATGTGGATGTCGCTGANGTTCATGACTGCTTTGCTN** AGAAATCTGGCCTGACACCAAATGATATTGACGTAATAGAACTTCACGATTGCTTTTCTA 465 AAAGCATTATTAAAATGGTTTGGCTTTGATATGAGTAAAGAAGCTGCAAGAAAATGCTATG ĠŦĠĊŦĠĊŦĠĊĊĊŦŦĂŦAGŦAŦĠŦĠAĀĠĊĀĞAĀAAĠĞĊŦĄĀAĠĀAŦŦŦĠŦĄĀAŦĄAĀĠAŦĠ TGGCATCTAAAGAAGTTTTTGATTTTTTGACTATCTTACAATGTTGTCCCACTTCAGATG **ACAGCAGAGAGAGCATAACAAGCTTAAAAGCTGCTAAAGTTGCAAGTGAAAAAGCATATA AAGCTGTGGAAATTTTGGCACAAGAAATGATGACTGATTTGCCAAGCTCGTTTGAAGAAA** GTGCTGCAGCAGTATTTTGGCCAGTGAAGCATTTGTACAGAAGTATGGCCTGCAATCCA Conservative 0, Score 92; DB 4; Pred. No. 2.6e-15 ed. No. 2.6e-15; Mismatches 300; Length 1664976; Indels -CAATTGCATTAC 1610166 15; Gaps 405 . 345 285 1610217 225 1610106 1610277 2

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Best Local Similarity
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US-08-232-463-14/c
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 bass
Type
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Patent No. 5670367
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                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: EP 9:
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F.G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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TOPOLOGY: lir
                                                                                                                                                                                                 TYPE: nucleic acid
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TELEFAX: (703)683-4109
                                                                                                                                       CLONE:
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1800 Diagonal Road,
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26-AUG-1991
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US-08-785-048-4
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                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1644 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                 FILING DATE: 27-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,8
MOLECULE TYPE:
                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 17-JAN-:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FASTSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/785,048
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MEDIUM TYPE: Diskette
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ADDRESSEE: SmithKline Beecham Corporation
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APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5763246el tRNA Synthetase
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                  TOPOLOGY: 1in
                                                                                                                                           TELEFAX:
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FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 9615
FILING DATE: 27-JUL-1996
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Best Local S
Matches 107
Query Match
Best Local Similarity 48.5
Matches 107; Conservative
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Patent No. 5965416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                        FILING DATE: 27-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P312
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hodgson,
APPLICANT: Lawlor,
TITLE OF INVENTION:
                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/7
FILING DATE: 17-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                          TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 709 Sw
CITY: King of
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 9601099.6 FILING DATE: 19-JAN-1996 APPLICATION NUMBER: 9615845.6
                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                            TELEFAX: 610-270-5090
                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
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          Score 39.8; DB Pred. No. 0.1; 0; Mismatches
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Pred. No. 0.1;
0; Mismatches 112; Indels
                                        DB 2;
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                                                                  Matches
                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/785,048 FILING DATE: 17-JAN-1997 CLASSIFICATION: 435
                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 27-JUL-1996
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 9601099.6
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 9615845.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: No. 5763246el tRNA Synthetase NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                              TYPE:
STRANDEDNESS: dou
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OPERATING SYSTEM:
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                               CCTCAGATGTTTGGGTATGCTGGAAAAGAACATATGGAAAAATATGGAACAAAAATTGAA
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יירופים acid
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                                                                             4.0%;
48.9%;
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                                                               Score 39.8; DE Pred. No. 0.1; 0; Mismatches
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US-08-996-799-1
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                                                                                                                                             Matches
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 27-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P313
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/785,048

FILING DATE: 17-JAN-1997

APPLICATION NUMBER: 9601099.6

FILING DATE: 19-JAN-1996

APPLICATION NUMBER: 9615845.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hodgson, John APPLICANT: Lawlor, Elizabeth TITLE OF INVENTION: No. 5965
                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1662 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                     STRANDEDNESS: double TOPOLOGY: linear
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ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 610-270-5090
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GAATACGAAATGGCTAAATTGAAAAATGATTTAGCAGAGTTCAATACGCATTTTGATAAT 771
                                CACTTTGCAAAAATTGGATGGAAAAATCATAAACATTCAGTTAATAACCCCGTATTCCCAG 134
                                                                    CCTGANATTAAAGATTATTCTGAAGAAGCACGTTTGAAAGAATTTAGAAAATTAGGCGTA
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                                                                                                                                          Score 39.8; DB 2; I
Pred. No. 0.1;
0; Mismatches 112;
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US-08-545-528D-1/c
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US-09-328-352-1034
                                                                                                                                                           Sequence 1034, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID ITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AN FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Fraser et al.
APPLICANT: INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB19 Ph
FILE REFERENCE: PB19 Ph
FILE REFERENCE: PB19 Ph
                                    NUMBER OF SEQ ID NOS:
SEQ ID NO 1034
LENGTH: 1368
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                      CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/08/545,528D CURRENT FILING DATE: 1995-10-19 PRIOR APPLICATION NUMBER: US 08/488,018 PRIOR FILING DATE: 1995-06-07 PRIOR APPLICATION NUMBER: US 08/473,545 PRIOR FILING DATE: 1995-06-07 NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Mycoplasma genitalium
          TYPE: DNA ORGANISM: Acinetobacter baumannii
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Local Similarity 52.7%;
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Pred. No. 2.
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RESULT 12
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Best Local S
Matches 70
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SEQ ID NO 1
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TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon,
Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION UMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
                                                                                                        sequence 1, Application US/08916421B
                                                                      NAME/KEY: misc_feature
LOCATION: (99266)..(98266)
OTHER INFORMATION: n equals a
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NAME/KEY misc_feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals
OTHER information: n equals
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OTHER INFORMATION: n equals
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LOCATION: (103998)..(103998)
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LOCATION: (84812)
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Similarity 56.9%;
70; Conservative
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(84773)..(84773)
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                             NAME/KEY: misc feature
LOCATION: (779455)...(779455)
OTHER INFORMATION: n equals
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a,
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a,
                                                                OTHER INFORMATION: n equals a,
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LOCATION: (741684)..(741684)
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LOCATION: (713652)..(713652)
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LOCATION: (682442)..(682442)
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals
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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a,
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LOCATION: (312837)..(3
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LOCATION: (191995)..(191995)
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LOCATION: (600992)..(600992)
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LOCATION: (312993)..(312993)
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INFORMATION: n equals
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          Sequence 13040, Application Patent No. 6551795
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: n equals
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LOCATION: (1569020)..(1569020)
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LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a,
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LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a,
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LOCATION: (871619)...(871619)
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LOCATION: (855539)..(855539)
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LOCATION: (1310988)..(1310988)
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OTHER INFORMATION: n equals a,
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LOCATION: (1664854)..(1664855)
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LOCATION: (1603734)..(1603734)
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LOCATION: (1602912)..(1602912)
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SEQ ID NO 12438
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APPLICANT: Marc J.
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Patent No. 6551795
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LENGTH: 1353
TYPE: DNA
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID AND AMINO TITLE OF INVENTION: AERUGINOSA FOR DIAGNOS EILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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CURRENT APPLICATION UMMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                            NAME/KEY: unsure LOCATION: (93), (101) OTHER INFORMATION: Identity of nucleotide at the above locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa FEATURE:
                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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Local Similarity 49.2%;
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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US-08-487-826B-13
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                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (619) 235-850
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 79; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-193
CLASSIFICATION: 435
CLASSIFICATION 1435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 09,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPHONE: (619) 235-8550
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APPLICANT: Sim, K
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MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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APPLICANT:
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TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
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STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                              3478 GAGCTATTAGCGGTAATTTAAAGTATTGTGAATTTTTCATTTAATATGCTATGATCATTT 3537
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172 CTAAAGAAGTTTTTTGATTTTTTGACTATCTT 202
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Miller, Louis H.
Peterson, David S.
Su, Xin-zhaun
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Db 3538 GATAATTAATTTTTTTTTATAATATTATATT 3568

Search completed: November 27, 2003, 12:32:29 Job time: 85.3681 secs

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Title:
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10100.295 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AR146582
methods for diagnosing and treating gastric cancer Patent: US 6218521-A 22 17-APR-2001;	Isolated nucleic acid molecules associated with gastric cancer and	Obata, Y.	1 (bases 1 to 843)	Unclassified.	Unknown.	Unknown.		AR146582.1 GI:15109771	AR146582	Sequence 22 from patent US 6218521.	AR146582 843 bp DNA linear PAT 08-AUG-2001	

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Stockert,E., Gure,A., Chen,Y.T., Gout,I.

OGHare,M., Obata,Y., Pfreundschuh,M., Tureci,O. and Sahin,U.
Concer-associated nucleic acids and polypeptides
Patent: JP 2001516009-A 497 25-SEP-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH
OS Homo sapiens (human)
JP 2001516009-A/497
PD 25-SEP-2001
PP 15-UUL-1998 JP 2000503425
PF 17-UUL-1997 US 08/980164,10-OCT-1997 US 60/061599 PR 10-OCT-1997 US 60/061765,10-OCT-1997 US 08/948705 PR 11-OCT-1997 US 60/061765,10-OCT-1998 US 09/102322 PI LLO
J OLD,MATTHEW J SCANLAN,ELISABETH STOCKERT,ALI GURE,YAO PI TS
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PC
G01N33/574,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K48/00,
A61P35/00,
PC
C07K14/82,C07K16/32,C12N15/09//C07K16/46,C12P21/08,A61K37/0
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Cancer-associated nucleic acids and polypeptides. FH
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JP 2001516009-A/497.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
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Sahin,U.
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                                                                                                                                                                                     Direct Submission
Submitted (24-JUN-1994) Jerome F. Strauss III, Department of Obstetrices and Gynecology, Division of Reproductive Biology, University of Pennsylvania Medical Center, 778 Clinical Research Building, 422 Curie Boulevard, Philadelphia, PA 19104-6142, USA
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1052)
Ohba, T., Rennert, H., Pfeifer, S.M., He, Z., Yamamoto, R.
Billheimer, J.T. and Strauss, J.F. III.
The structure of the human sterol carrier protein X/s
protein 2 gene (SCP2)
Genomics 24 (2), 370-374 (1994)
                                                                                                                                                                                                                                                                                                    2 (bases 1 to 1052)
Strauss, J.F. III.
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1052 bp DNA
Human sterol carrier protein-X/sterol carr
(SCP-X/SCP-2) gene, exon 16, and complete
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                                                                                                                                                                        Location/Qualifiers
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carrier protein-2
lete cds.
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      .108, U11300.1:1.
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      TGGATTGGGGAAAAAATNCNGTTCCNNATACCNNGAANNGCAAANTTTTTAAATTTTTA
                                                                      AAAANTNITTTNATTTTAAAAATAACCCCNGTNTCCAACCCCCNGATCANATTCCTTTNATT
                                                                                                                                                           ATCCTNAANGAGGGNNTTTNANNACTAATNCCCNGATTTTCCAATANGGAANCCCNNNTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCCAGAAAAAGTTATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCC
                                                                                                                              ATTCTTAATGATGGTGTTTTATGACTAATACACTGATTTTTCAATAAGGAAACCCATGTT
                                                                                                                                                                                                                    <u>AAATTGAAATGAGATTATAATTTGAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATT</u>
                                                                                                                                                                                                                                                          AATTNGAANTNAAATTATANTTNGAAANCGGCNNCNGAAACCAANCTTNATGGTCCAATT
                                                                                                                                                                                                                                                                                                      ATGCAGATAATTAAACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTAT
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TGKWNPQSAFFQGKLKITGNWGLAMKLQNLQLQPGNAKL"
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U11304.1:26. .89,U11305.1:26. .112,U11306.1:26. .176,

U11307.1:26. .173,U11308.1:26. .133,U11309.1:1547. .11

U11310.1:26. .128,U11311.1:26. .155,U11312.1:26. .105,
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157 c
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Pred. No. 1.1e-93;
); Mismatches 233
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421

coverage: 3.75x in Q20 bases; agarose-fp

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Insert size: 121476; sum-of-contigs
Insert size: 136681; 7.7% error; agarose-fp
Quality coverage: 4.05x in Q20 bases; sum-of-contigs Quality
                                                                           Assembly program: XGAP4; version 4.5 sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator ET-amersham; 20% of read Dye-terminator Big Dye; 79% of reads Consensus quality: 118880 bases at least Q40 Consensus quality: 120216 bases at least Q30 Consensus quality: 120979 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
on Aug 12, 2000 this sequence version replaced gi:9214208.
                                                                                                                                                                                                                                                                                         Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL358233 GI:9797852
AL358233.3 GI:9797852
HTG; HTGS_PHASE1; HTGS_CANCELLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL358233 122176 bp DNA 1
Homo sapiens chromosome 1 clone RP5-835A17,
PROGRESS ***, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTTNCNGGCCACCNGTGGGCNTNGTNTTCCTTACTTANTCCCCCCAAGGAAANNCCTTAA
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SEQUENCING IN
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                                    ATGCAGATAATTAAACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTAT
                                                                 TNGCAAATANTTAACCTTNCTTGAAAANGGAAATTTNTACCAANGGACNGAAANCNTTNT 180
                                                                                                                                                           TATNNCNCNCNGANTTTNANAAANTACCTTTNNTNTTAAAAAAACCTNGGAAAAAAAATAA 120
                                                                                                                                                                                                                                                  GGCCAAAAAAANTTATTINAATTTCCTATTAANCNTCCTCCNCAAANCATTATTINACCC
                                                                                                                                                                                                                          GGCCAGAAAAGTTATTTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCC
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6: gap of 100 bp
3: contig of 17307 bp in length
3: gap of 100 bp
2: contig of 6029 bp in length
2: gap of 100 bp
1: contig of 8259 bp in length
1: gap of 100 bp
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1: gap of 100 bp
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RESULT 4 AL358233

COMMENT

Center: Sanger Centre Center code: SC

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Center project name: dJ835A17

REFERENCE

AUTHORS TITLE JOURNAL

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SOURCE KEYWORDS VERSION ACCESSION DEFINITION

ORGANISM

Homo sapiens

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collims, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
                                                                                                                                                                                                                                                                                                                                           Homo sapiens chromosome 1 clone
SEQUENCE, 34 unordered pieces.
AC022728
AC022728.4 GI:7249198
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                    Homo sapiens chromosome 1, Unpublished
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 175046)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 1, clone RP11-310J14
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COMMENT

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence

consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Care between the property of the pieces of the pieces is not known and their order in this sequence record is

NOTE: This is a 'working draft' sequence. Quality coverage: 3.4 in Q20 bases; Quality coverage: 3.6 in Q20 bases;

sum-of-contigs agarose-fp

It currently

as soon as it is available and the accession be preserved.

157

56: 156: 1191:

contig of 56 bp in length gap of 100 bp contig of 1035 bp in leng

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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Collins, S., Colmopoiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Debarellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreita, P., FitzHugh, W., Gage, D., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Piesni, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stolaner, S., Severy, P., Spencer, B., Stange-Thomann, N., Scolanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 16, 2000 this sequence version replaced gi:6980310.
All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young, G., Zainoun,
Direct Submission
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Center project name: L5491
Center clone name: 310 J 14
Center clone name: 310 J 14
Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 156135 bases at least Q30
Consensus quality: 165373 bases at least Q30
Consensus quality: 165370 bases at least Q30
Consensus quality: 165370 bases at least Q30
Consensus quality: 165370 bases at least Q30
Insert size: 185000; agarose-fp
Insert size: 171746; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
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REFERENCE

AUTHORS

gap of contig gap of contig

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/organism="Homo sapiens"
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                                                                                                                                                                 Jagor gap of 100 bp

36738 contrig of 4438 bp in length

36838 gap of 100 bp

43447 contrig of 6609 bp in length

43547 gap of 100 bp

48625 contrig of 4978 bp in length

48625 gap of 100 bp

52891 gap of 100 bp

58391 contrig of 6378 bp in length

58491 gap of 100 bp

64969 gap of 100 bp

64969 gap of 100 bp

81101 contrig of 6378 bp in length

73469 gap of 100 bp

81101 contrig of 632 bp in length

81201 gap of 100 bp

87754 contrig of 653 bp in length

98534 gap of 100 bp

98534 contrig of 653 bp in length

98534 contrig of 653 bp in length

98534 gap of 100 bp

102797 contrig of 7680 bp in length

102897 gap of 100 bp

111917 gap of 100 bp

111917 gap of 100 bp

112160 contrig of 8920 bp in length

111917 gap of 100 bp

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14949: contig of 1451 bp in 18
15049: gap of 100 bp
16260: contig of 1211 bp in 18
16360: gap of 100 bp
18265: gap of 100 bp
18365: gap of 100 bp
18365: gap of 100 bp
18365: gap of 100 bp
20916: contig of 1951 bp in 18
20016: gap of 100 bp
22939: contig of 2923 bp in 18
23039: gap of 100 bp
26445: gap of 100 bp
26445: gap of 100 bp
26447: gap of 100 bp
29327: contig of 3406 bp in 18
29327: contig of 3782 bp in 18
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9001: contig of 1349 bp
9101: gap of 100 bp
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contig of 1052 bp i
gap of 100 bp
contig of 1379 bp i
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contig of 2773 bp
gap of 100 bp
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contig of 1462 bp
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f 100 bp
g of 1114 bp
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                          ATTACTGGCCAGCTGTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGAAAACTCTTAA
                                                              NTTNCNGGCCACCNGTGGGCNTNGTNTTCCTTACTTANTCCCCCCAAGGAAANNCCTTAA 539
                                                                                                                        ACCCCCCTANTTTTAAAANCTATNGAAAANTNGATTANNGACTTGAATTGC-CAACCCTA
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157. .1191
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D; Mismatches 233;
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FEATURES source

Location/Qualifiers

/mol_type="genomic_DN /db_xref="taxon:9606" /chromosome="1"

81102 81202 87755 87855 95535 95635 102798 1102898 1111918 1111918 121161 121161 121261 140638

52892 58392 58492 64870 64970 73370 73470

26546 29328 29328 29428 29428 32201 32201 336739 36739 43448 433448 43548

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source
                                                                                                                                                                                                                                                     Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 7, 2002 this sequence version replaced gi:17939714.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows under the noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em. EMBL; Sw.,
SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP
database can be found at
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                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
                                                                    of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                             RP11-334A14 is from the library RPCI-11.2 constructed
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                  //www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vesa,J., Hellsten,E., Branoski,B.L., Emanuel,B.S., Billheimer,J. Mead,S., Cowell,J.K., Strauss,J.F.III. and Peltonen,L. Assignment of sterol carrier protein X/sterol carrier protein 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       He,Z., Yamamoto,R., Purth,E.E., Schantz,L.J., Naylor,S.L., George,H., Billheimer,J.T. and Strauss,J.F. III. cDNAs encoding members of a family of proteins related to hur sterol carrier protein 2 and assignment of the gene to human
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Best Local Similarity
Matches 606; Conserv
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 187
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 432978.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: ht
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens, sterol ca.
IMAGE:4287946, mRNA, co.
BC005911
BC005911.1 GI:13543502
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Mammalia; Eutheria; Primates;
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                                                                                                                        NCNCNGANTTTNANAAANTACCTTTNNTNTTAAAAAACCTNGGAAAAAAATAATNGCAA 126
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 AANTNAAATTATANTTNGAAANCGGCNNCNGAAACCAANCTTNATGGTCCAATTATCCTN
                               ATAATTAAACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAAATTG 1227
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EQPVKKIGGIFAFKVKDGFGGKEATWVDVKNGKGSVLENSDKKADCTIIWADSDFLA
LMTGKMNPQSAFFQGKKITGNMGLANKLQNLQLQPGNAKL"
1 219 c 272 g 458 t
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/product="sterol carrier protein
/protein_id="AAH05911.1"
/db_xref="GI:13543503"
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/db_xref="LocusID:6342"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
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AR146579
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G01N13/574,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K48/00,
PC G07K14/82,C07K16/32,C12N15/09//C07K16/46,C12P21/08,A61K37/0
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PC C12N15/00
CC Cancer-associated nucleic acids and polypeptides. FH Key
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/mol_type="genomic DNA"
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G01N35/00
PC C07K14/82,C07K16/32,C12N15/00
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10-OCT-1997 US 60/061765,10-OCT-1997 US 08/948705 PR
11-OCT-1997 GB 9721697.2,22-JUN-1998 US 09/102322 PI
J OLD, MATTHEW J SCANLAN, ELISABETH STOCKERT, ALI GURE, YAO PI
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OGhare,M., Obata,Y., Pfreundschuh,M., Tureci,O. and Sahin,

Cancer-associated nucleic acids and polypeptides

Patent: JP 2001516009-A 495 25-SEP-2001;

LUDWIG INSTITUTE FOR CANCER RESEARCH

OS Homo sapiens (human)

PN JP 2001516009-A/495

PD 25-SEP-2001

PF 15-JUL-1998 JP 2000503425

PR 17-JUL-1997 US 08/896164_10-OCT-1997 US 60/0615
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1 (bases 1 to 687)
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                                                  /translation="MGFPEAASSFRTHQIEAVPTSSASDGFKANLVFKEIEKKLEEEG
EQFVKKIGGIFAFKVKDGPGGKEDTWVVDVKNGQGSVLFNSDKKADCTITMAASDFLA
LMTGKMNPQSAFFQGPLKITGNMGLAMKLQNLQLQPGNAKL"
                                                                                 /codon_start=1
/product="sterol carrier
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/db_xref="GI:263551"
                                                                                                                                                             gene="sterol
                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                            note="This sequence
                                                                                                                                      gene="sterol carrier protein 2,
                                                                                                                                                                                                      organism="Homo sapiens"
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TATCCCACGCTATTTGCCGATGTGTAGTTTCAGTCTAAATTCTGACAATAAAATG
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Vesa,J., Hellsten,E., Branoski,B.L., Emanuel,B.S., Bliller,C., Vesa,J., Hellsten,E., Branoski,B.L., Emanuel,B.S., Bliller,C., Wead,S., Cowell,J.K., Strauss,J.F.III. and Peltonen,L. Mead,S., Cowell,J.K., Strauss,J.F.III. and Peltonen,L. Messignment of sterol carrier protein 2 Assignment of sterol carrier protein 2 Assignment of sterol carrier protein 2 and exclusion as the causative gene for infantile neuronal 1p32 and exclusion as the cesoid lipofusionosis Cloning and expression of a cDNA protein 2 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1219) sterol carrier protein-2. Homo sapiens (human) Yamamoto,R., Kallen,C.B., Babalola,G.O., Billheimer,J.T. and Strauss,J.F. III. M55421.1 GI:432978 Proc. Natl. Acad. Sci. U.S.A. Homo sapiens Human sterol carrier (bases 1 to 1219) يا 1219 pp د protein-2 (د 88 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. p mRNA (SCP-2) n (2), 463-467 encoding mRNA, Rennert, H. human linear complete (1991) Billheimer, J.T., PRI 06-DEC-1993 carrier ç

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CTTAANTATCCTTGGTAACCAAANCAAAACCTTTTTNGTTTACNTANTCCTTGGGATTTA
                                                       GTGTTTCTTACTTAGTTCTCCCAAGGAAAACTCTTAAACTGAATCTTCAGCAGAATAATC
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/evidence=not_experimental
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EQFVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPNSDKKADCTITMADSDFLA
LMTGKWNPQSAFFQGKLKITGNMGLAMKLQNLQLQPGNAKL"
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/evidence=experimental
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/product="sterol carrier protein-2"
/protein id="AAA03559.1"
db_xref="GI:432973"
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/mol_type="mRNA"
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Mead,S., Cowell,J.K., Strauss,J.F.III. and Peltonen,L.
Assignment of sterol carrier protein X/sterol carrier protein 2
1932 and exclusion as the causative gene for infantile neuronal
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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al source text: Human liver cDNA to mRNA.
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                                   DVKNGKGSVLPNSDKKADCTITMADSDFLALMTGKMNPQSAFFQGKLKITGNMGLAMK
LQNLQLQPGNAKL"
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                                                                                                                                                          /product="sterol carrier protein-2"
/protein_id="AAA03558.1"
/db_xref="GI:432977"
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/gene="SCP-2"
/note="no polyA
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/mol_type="mRNA"
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Search completed: November 27, 2003, 10:02:41 Job time: 3416.44 secs

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Listing first 45 summaries
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ALIGNMENTS

REFERENCE AUTHORS TITLE SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1
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LOCUS
DEFINITION COMMENT JOURNAL wx25e05.xl NCI CGAP Kidll Homo sapiens cDNA clone IMAGE:2544704 3' similar to gb:S52450 NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (HUMAN);, mRNA sequence. Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D. Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertel
Mammalia; Butheria; Primates; Catarrhini; Hom.
1 (bases 1 to 786)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anator AW052045.1 GI:5914404 CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be cound through the I.M.A.G.E. Consortium/LLNL at: Homo sapiens (human) Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. Anatomy Ph.D., Project Michael R. (CGAP),

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Seq primer: -40UP from Gibco
High quality sequence stop: 458.
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UNAACCATANTTACCATTTTACCTTGGTAAGGCNCAGTNGTTTGCANTNCCGCAAANCAG
                                     GTTTACATAGTTCTTTGGATTTTACTGTTCCTAATTATATTCTGAAACTCAATTTTACCC
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Location/Qualifiers
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/note="Organ: kidney; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI_CGAP Kid3 was prepared, and ss.circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132376-132391), 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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116 c 109 g
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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RESULT 2
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Mammalla; Eutheria; Primates; C
1 (bases 1 to 953)
Li,W.B., Gruber,C., Jessee,J. a
Full-length cDNA libraries and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Faraday Avenue Genoscope sequence ID : CS0DK001CF01NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cgi-bin/cluster.cgi?seq=CSODK001CF01NP1&cluster=268.f. Contact Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 268.f more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Feb 16, 2001 thi
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BP 191 91006 EVRY cedex - France
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                                TTGAAAANGGAAATTTNTACCAANGGACNGAAANCNTTNTAATTNGAANTNAAATTATAN 200
                                                                       GAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAATGCAGATAATTAAACTTAC
                                                                                                   AAANTACCTTTNNTNTTAAAAAAAACCTNGGAAAAAAATAATNGCAAATANTTAACCTTNC 140
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ATGĀĀĀĀAAGGĀĀĀATTATĀACĀĀAAGGACTGAGĀACGTTATAAATTGĀAAATGAGATTATAA 182
                                                                                                                                              AKKKGHDNTTAAACATTCTTCTCAAAGCATTATTTTATCCTATATCTCACTGAATTTTAA 62
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/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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70.4%;
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Pred. No. 3.4e-79;
7; Mismatches 232
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Catarrhini; Hominidae;
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RESULT 3
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Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 268.f
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi/seq=CSOBAKO54BDO7NM1&cluster=268.f. Cont.
Feng Liang Email: fliang@lifetech.com URL:
http://tulllength.invitrogen.com/ InVitroGen Corporation 160.
Faraday Avenue Genoscope sequence ID: CSOBAKO54BD07NM1.
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                                                                                                                                                                      Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                               Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; (bases 1 to 901)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Location/Qualifiers
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//note="Organ: kidney; Vector: pT773D-Pac (Pharmacia) with
/note="Organ: kidney; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 132376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo. "
96 a 128 c 114 g 278 t 5 others
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                                    University of Iowa
2024 University of Iowa
Tel: 319 356 4866
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      Email: paul-mccray@uiowa.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (www.openbiosystems.com).
The following repetitive elements were found in this cDNA sequence: 316-342, >AT rich#Low_complexity (matched compliment) Seq_primer: M13 FORWARD
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TAG_SEQ=AAGTGCTTAC"
107 c 97 g
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TAG_TISSUE=Normal Lung
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/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_llb="UI-CF-EC1"
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mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LINI at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 316-342, >AT_rich#Low_complexity (matched compliment)
Seg primer: M13 FORWARD
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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VI-H-ED0-axo-f-03-0-VI.s1 NCI_CG
IMAGE:5831426 3', mRNA sequence.
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Contact: Robert Strausberg,
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/clone lib="NCI (GAP_ED0"
/clone lib="NCI (GAP_ED0"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
/pharmacia) with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCI (GAP_ED0 is a CDNA library containing
the Following tissue(s): Chondrosarcoma cell line CS5. The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
CDNA synthesis was primed with an oligo-dT primer
                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                /clone="IMAGE:5831426"
/tissue_type="Chondrosarcoma"
                                                                                                                                                                                                                                                                                db_xref="taxon:9606"
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_LIB=UI-H-ED0
TAG_TISSUE=chondrosarcoma
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밁 Ś 밁 5 В Ś 밁 Ş 밁 Ś В δ 밁 Ş 밁 Ş 밁 Ś В Ś 뮍 Ś 밁

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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library preparation: Dr. M. Bento Soares, University of Iow CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://inage.llnl.gov The following repetitive elements were found in this cDNA sequence: 317-343, >AT rich#Low_complexity (matched compliment) Sequence: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UI-H-ED1-axs-g-24-0-UI.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone IMAGE:5833007 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AATTNGAANTNAAATTATANTTNGAAANCGGCNNCNGAAACCAANCTTNATGGTCCAATT 240
                                              ATGCAGATAATTAAACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTAT
                                                                                TNGCAAATANTTAACCTINCTIGAAAANGGAAATTINTACCAANGGACNGAAANCNTINT 180
                                                                                                                                                                       TATNNCNCNCNGANTTINANAAANTACCITTNNTNTTAAAAAACCINGGAAAAAAATAA 120
                                                                                                                                          TATATCTCACTGAATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAA
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nilarity 72.7%;
Conservative
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/lab host="DH10B (Life Technologies)"
/clone lib="NCI_CGAP_ED1"
/clone lib="NCI_CGAP_ED1"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(pharmacia) with a modified polylinker; Site_1: BCOR I;
Site_2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line CS5. The library was constructed according to Bonaldo
.Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT7T3-Bac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT) B tail. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_LIB=UI-H-ED1
TAG_TISSUE=chondrosarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence tag for this library is GCTCAAGGCT.
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'db_xref="taxon:9606"
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Pred. No. 1.8e-7
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University of Iowa
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SOURCE
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                                                                  Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 268.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.gi?seq=CSOBAKO77DD07NM1&cluster=268.f. Contact:
Feng Liang Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAKO77DD07NM1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 905)
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                                                                                                                                                                                                                                                                                                                        Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
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BX414370.1 GI:30637003
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                  ACAACCTTCCCCCNCC----TTTGGCCCAGGNNTTNTTCCCGTCTAAATCCGAACAATAA
                                                                                                           CCATCAGGCTCTATTTACCCCAGAGCATAGGAAAAACAGGATTGGTCACACCCATTAAGAA
                                                                                                                                            cccneg---cnctttcccccganccttgggaaaaacgggatnggtccccccttaaaaa
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/tissue_type="FETAL LIVER"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/clone_lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDh was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."

136 c 123 g 312 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consorthum/LLNL at:
www.bio.llnl.gov/bbrp/image/image.hrml
Insert Length: 1454 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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National Cancer Institute, Cancer Genome Anat
'ATTNGAANTNAAATTATANTTNGAAANCGGCNNCNGAAACCAANCTTNATGGTCCAATTA 241
                                             TGCAGATAATTAAACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATA
                                                                        NGCAAATANTTAACCTTNCTTGAAAANGGAAATTTNTACCAANGGACNGAAANCNTTNTA 181
                                                                                                                              ATATCTCACTGAATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAGATAAA 144
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         /note=Torgan: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(GT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

39 9 285 t 4 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2417221"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="normal prostate"
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72.5%;
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Pred. No. 4.7e-76;
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                                                                                                                   Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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                                        Insert Length: 654 Std Error:
Seq primer: -40UP from Gibco
High quality sequence stop: 458
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1 (bases 1 to 793)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                   found through the I.M.A.G.E. Consortium/LLNL
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 654 Std Error: 0.00
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                                CAGACCCATAATACCCATATAACTTTGTAATGCACAGTTGTATGCAATTTCGCAAAGCAG
                                                                                                  G-TTACATAGTTCTTTGGATTNTACTGGTCCTAANTTTATTCTGAAACTCAATTNTACCC
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                                                            CNAACCATANTTACCATTTTACCTTGGTAAGGCNCAGTNGTTTGCANTNCCGCAAANCAG
                                                                                                                                                                                                                                 ATTACTGGCCAGCTGTTGGCATTGTGTTTTCTTACTTAGTTCTCCCAAGGAAAACTCTTAN
                                                                                                                                                                                                                                                                                                   ATCTCACTAATTTTAAGAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NCI_CGAP_Kid11"

/note="Organ: kIdney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2171984"
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71.0%;
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Pred. No. 1.4e-75;
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TITLE
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Matches 537; Conserv
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782 ATAAGAAACAA 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA sequence: 1-43, xAT rich#Low complexity (matched compliment) 309-335, xAT rich#Low complexity (matched compliment) Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BU627147
UI-H-FG0-bct-i-12-0-UI.sl NCI CGAP EN1 2 Homo
UI-H-FG0-bct-i-12-0-UI 3', mRNA sequence.
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                         /Clone_lib="NCI_CGAP_ENI_2"
//Clone_lib="NCI_CGAP_ENI_2"
//Clone_lib="NCI_CGAP_ENI_2"
//Clone_Togan: Bone; Vector: pTTJ3-Pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I; NCI_CGAP_ENI_2 is a cDNA library containing the following tissue(s): Enchondroma cell line (2 cell lines). The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strandd cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pTTJ3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGGTCACTC. The cell lines was provided by Dr James Martin from University of Iowa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene Index
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                                                                                                                                 TAG_LIB=UI-H-FGO
TAG_TISSUE=Enchondroma cell line (Mix of ENI
TAG_TSSQ=CGGTCACTC"
TAG_SEQ=CGGTCACTC"
109 c 97 g 286 t l others
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db_xref="taxon:9606"
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54.8%;
72.7%;
   Score 462.2; DB 13; Pred. No. 2.4e-75;
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     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                              Unpublished
Contact: Robert Strausberg,
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 824)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
BE738457
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824 bp mRNA linear EST 15-St 601572489T1 NIH_MGC_57 Homo sapiens cDNA clone IWAGE:3839159
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM527 row: b column: 24
High quality sequence stop: 762.
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     AAGCTTTTTTGTTTACATAGTTCTTTGGATTTTACTGTTCCTAATTTTATTCTGAAACTC
                                                     AACCTTTTTNGTTTACNTANTCCTTGGGATTTAACGGGTCCCCAATTTNATCCNGAACCC
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/lab host="DH10B (TI phage-resistant)"
/clome lib="NIH_MGC_57"
/clome lib="NIH_MGC_57"
/clome lib="NIH_MGC_57"
/forte="Organ: brain; Vector: pDNR-LIB (Clontech); Site 1:
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site 1:
/forte="Organ: brain; Clontech from cell line RNA. 5:
/forte="Organ: brain; Site 1:

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/db_xref="taxon:9606"
/clone="IMAGE:3839159"
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70.8%;
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Pred. No. 5.9e-75;
D; Mismatches 227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Setteribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 316-342, AAT_rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 759)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BU619112 759 bp mRNA linear EST 23-SEP-2002 UI-H-FH1-bfm-l-10-0-UI.81 NCI_CGAP_FH1 Homo sapiens cDNA clone UI-H-FH1-bfm-l-10-0-UI 3', mRNA sequence.
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             /clone lib="NCI CGAP FHI"
//clone lib="NCI CGAP FHI"
//note="Organ: Chondrosarcoma; Vector: pT7T3-Rac (Pharmacia / note="Organ: CGAP FHI is a normalized cDNA library obtained from a cell line derived from grade I chondrosarcoma tissue. The library was constructed and normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAATCCGGC. The cell line was provided by Dr. James Martin from the University of
                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Adult"
/lab_host="DH10B_(Life_Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                  /clone="UI-H-FH1-bfm-l-10-0-UI"
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Chinese National Human Genor
351 Guo Shoujing Road, Zhan
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
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Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu
,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z. and Han,Z.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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lone is available at CHGC
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="HTCCAD08"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 738)
Bonaldo, M.F., Lennor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The following repetitive elements were found in this sequence: 316-342, >AT rich#Low_complexity (matched co Seg primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McCray Lab
University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8889548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9), 97044477
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Tel: 319 356 4866
Fax: 319 356 7171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Normalization and subtraction:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (www.openbiosystems.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCTATTCACCCAGAGCATAGGAAAAAACAGGATTGTCACACCCCATTAAGAA
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dev stage="Adult"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="U1-CF-EN1"
/clone Tib="U1-CF-EN1"
/clone Tib="U1-CF-
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTNCNGGCCACCNGTGGGCNTNGTNTTCCTTACTTANTCCCCCCCAAGGAAANNCCTTAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAATATTTTTATTTTAAAAATAAGCCTGTGTTCAAGCTCTGATCATATTTCTTTTATTT
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                                                                                                                                                                                                                              TTTACHTANTCCTTGGGATTTAACGGGTCCCCAATTTNATCCNGAACCCANTTTTCCCCC
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AGACCATGATTACCATATTAACTTTGGTATGCACAGTTGTATGCATTCC
                                                                                                                                                     TTTACATAGTTCTTTGGATTTTACTGTTCCTAATTTTATTCTGAAACTCAATTTTACCCC
                                                                                                                                                                                                                                                                                                               CTGAATCTTCAGCAGAATAATCCTTAAATATACTTTGTGAGCAAAACAAAAGCTTTTTTG
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TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h

TAG_SEQ_CTGCTCAGGT"

TAG_SCCTCGCTCAGGTTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTTAGGTTAGGTTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTAGGTTA
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Search completed: November 27, Job time: 2274.04 secs

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seq length: 2000000000
N Geneseq 19Jun03;*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ABABJU93	AAH57293	AAT19975	ABV87267	AAX40095	AAX40094	AAH57501	AAX40097	DB ID
corn ear-derived p	Human liver specif	Human gene signatu	Human colon cancer	Gastric cancer ass	Gastric cancer ass	Human liver cell s	Gastric cancer ass	Description

Chemically treated	ABL54306 ABL32157 ABL33169	2222	7049 7049 7781 37515	л 5 5 5 1 7 7 7	48.2 48.2 47.8	4 4 4 4 0 4 4 0 0 4 0	იიიი
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Human immune sys Human immune sys Human metastasis	ABL32336 ABL34146 ABL34575	2221	7201 15667 17491		4 4 4 6 8 8 8 6 4 4 6	i	0000
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ALIGNMENTS

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RESULT 1
AAX40097
ID AAX4
22-JUN-1998;
17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                                                                  Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer; prostate cancer; ss.
                                                                                                            28-JAN-1999.
                                                                                                                                                                                                       Gastric cancer associated gene.
                                                                                                                                                                                                                         02-JUL-1999
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                                                                                           15-JUL-1998;
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                                                                                                                                                 Homo sapiens.
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       (LUDW-) LUDWIG
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97US-0061599.
97US-0061765.
97US-0948705.
97GB-0021697.
       INST CANCER RES
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Query Match
Best Local Similarity
Matches 843; Conser
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                        sequences (1). (1) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (1) and proteins (11) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (1) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (1) and (11) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a prognosis or monitoring of treatments and for investigating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology -
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             standard;
                                                                                                                                                                                                  TANTNITICE -- CCNGGCNCTTTCCCCCGANCCTTGGGAAAAACGGGATNGGTCCCCCCCT
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Pred. No. 9.5e-110;
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17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                                                                                                                                                         The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated cancer associated nucleic acids and polypeptides isolated using sera from cancer patients, used to develop profor the diagnosis, monitoring or treatment of cancers
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Pred. No. 5.8e-94;
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Pfreundschuh
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, remal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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CAT-TTTACCTTGGTAAGGCNCAGTNGTT
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                                                              TGGGATTTAACGGGTCCCCAATTTNATCCNGAACCCANTTTTCCCCCCNAACCATANTTAC
                                                                                                                             AAAATAACCCTTAANTATCCTTGGTAACCAAANCAAAACCTTTTTNGTTTACNTANTCCT
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                                             TTGGATTTTACTGTTCCTAATTTTATTCTGAAACTCCATTTTTCCCCCAGACCATAATTAC
                                                                                                    NGAATAACCTTAAATATACTTTGTTAGCCAAAC---
                                                                                                                                                            GTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGAAAACTCTTAAACTGAATCTTCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 695; 787pp;
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71.8%;
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Pred. No. 3.5e-88;
0; Mismatches 190
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                 701
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                                                                                                                                                                                                                           The invention relates to a human colon tumour expressed polynucleotide (I) encoding a polypeptide (II, ABP67991-ABP87996) comprising; (i) any of 2600 fully defined nucleotide sequences (ABV8669-ABV89289); (ii) complements of (i); (iii) at least 20 contiguous residues of (i); (iv) sequences that hybridize to (i), under moderately stringent conditions; (v) sequences having at least 75% or 90% identity to (i); or (vi) degenerate variants of (i). The compositions and methods of the present invention are useful for the diagnosis, prevention and/or treatment of cancer, particularly colon cancer. (I) can be used in gene therapy and (I) and (II) are useful in pharmaceutical compositions such as vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated tumor colon polynucleotide and polypeptide, useful diagnosis, prevention and/or treatment of cancer, in particular cancer -
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
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06-FBB-2001; 2001US-26701P.
28-MAR-2001; 2001US-279670P.
10-JUL-2001; 2001US-304037P.
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                     GCAAATANTTAACCTTNCTTGAAAANGGAAATTTNTACCAANGGACNGAAANCNTTNTAA 182
                                                                   TNNCNCNCNGANTTTNANAAANTACCTTTNNTNTTAAAAAAACCTNGGAAAAAAAAATAATN
                                                                                                     CCAGAAAAGTTATTTTAATTTTCTATTAAATATTCTTCTCAAAGCATTATTTTATCCTA
                                                                                                                    CCAAAAAANTTATTTNAATTTCCTATTAANCNTCCTCCNCAAANCATTATTTNACCCTA
                                                                                                                                                                                                        486 BP; 192 A;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 578;
GCAGATAATTAAACTTACATGAAAAAGGAAAATTATAACAAAGGACTGAGAACGTTATAA
                                                  TATCTCACTGAATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAAT
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J,
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                                                                                                                                                                 Score 313.6; DB Pred. No. 6.1e-65
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                                                                                                                                                                                                        64 G; 175 T; 0 other;
                                                                                                                                                      Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                tissues
                                                                                                                                                                                                                                                                                                                                                                                                  Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-1994;
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                                                                                                                                                                                                                                                                                                                      525;
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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAR19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each libraries all the 3'-oriented cDNAs hybridise with specific mRNAs.

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Best Local
   Claim 1; Page 117; 327pp; English
                               New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology -
                                                                                              WPI; 2001-291057/30.
                                                                                                                                                                                                                                                                                                                                                     lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
metabolic disease; developmental disease; cytostatic; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              different mRNAs in the particular tissue from which it was derived The appearance frequency of a given GS in a CDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                  02-NOV-2000; 2000WO-US30396
                                                                                                                                                                                                                                                                                                                                                                                     Human; tissue specific; diagnosis; brain; heart;
                                                                                                                                                                                                                                                                                                                                                                                                                   Human liver specific cDNA sequence SEQ ID NO:133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 351 BP; 117 A; 44 C; 44 G; 141 T; 5 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATNGCAAATANTTAACCTTNCTTGAAAANGGAAATTTNTACCAANGGACNGAAANCNTTN 179
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                                                                                                                                                         GENOMICS INC
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73.6%;
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Pred. No. 6.8e-42;
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                                                                                                                                                                                                                                                                                                                                                                                     skeletal muscle;
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Best Local S
Matches 195
                                                                                                                                                                                                                                                                                                                      Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SATMON023; structural gene; functional gene; regulatory gene; corn ear-specific profile; gene transcription; gene expression hybrid plant; desirable trait expression; plant breeding progrinheritance; desired characteristic; growth; development;
                                                                                                                                                                                                                                                                                              disease resistance; environmental adaptability; quality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-2003
                                                                       14-MAY-1999;
                                                                                                                                                                        US6476212-B1
                                                                                                                                                                                                                                                                       multigene trait;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corn ear-derived polynucleotide (cpd)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABX83093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABX83093 standard; cDNA; 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                       99US-0313294
                                                                                                                                                                                                                                                                       plant; gene; ss.
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74.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
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                                                                                                                                                                                                                                                                                                                                                                             expression;
                                                                                                                                                                                                                                                                                                    yield;
                                                                                                                                                                                                                                                                                                                                                program
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26-MAY-1998;

98US-086722P

(INCY-)

INCYTE GENOMICS INC

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RESULT 9
ABX40797
ID ABX4
XX
AC ABX4
XX
DT 20-F
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BOV1
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KW BOV1
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KW BOV1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC functional, and regulatory genes of corn ear. The polynucleotides are useful for detecting code in a sample, for producing CC altered gene expression in inbred or hybrid plants, and for screening CC altered gene expression in inbred or hybrid plants, and for screening CC are useful to identify, isolate, or extend identical or related CC corn-ear nucleic acid sequences from DNA libraries, and in nucleic acid amplification or hybridisation techniques to follow the expression of desirable traits through plant breeding programs. CC preferably, the cdps are used to identify, evaluate, alter, or cc follow the inheritance of desired characteristics associated with CC growth and development, disease resistance, environmental adaptability, CC quality, and yield of corn. The cdps are also useful as molecular CC polypeptides by recombinant techniques. They are also useful in CC diagnostic assays to detect or confirm conditions or diseases CC associated with abnormal levels of cdp expression. ABX81541-ABX89140 CC represent corn ear-derived polymucleotides (cpds) of the invention. CC USPTO web site at sequata.uspro.gov/psipsDIDEntry.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                 gene analysis; cattle breeding
                                                  Bovine, 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene i
                                                                                                       Bovine EST associated with lactation/muscle/fat deposition
                                                                                                                                                                                                                  ABX40797 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 173 BP; 54 A; 20 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel purified corn-ear derived polynucleotide useful as hybridization probe for detecting polynucleotide in sample, and for identifying, evaluating, and altering desired characteristics associated with
 Bos Taurus
                                                                                                                                            20-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SATMON022 and SATMON023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Loca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to the isolation of corn ear-derived ynucleotides (cdps) from the corn (Zea mays) cDNA libraries MON022 and SATMON023. Some of the cpds uniquely identify struct
                                                                                                                                                                                                                                                                                                                                                                                112
                                                                                                                                                                                                                                                                                                                                            128
                                                                                                                                                                                                                                                                                                                                                                                                                                                       172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                            TANTTAACCTTNCTTGAAAANGGAAATTTNTACCAANGGACNGAAANCNTT 178
                                                                                                                                                                                                                                                                                                                                                                                CACTGAATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAATGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                   CNCNGANTTTNANAAANTACCTTTNNTNTTAAAAAACCTNGGAAAAAAAATAATNGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAAGTTATTTAATTTTCTATTAAACATTCTTCTCAAAGCATTATTTTATCCTATATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID No 1553; 390pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                         (first entry)
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                                                                                                                                                                                                                CDNA; 397
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71.3%;
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                                                                                                                                                                                                                    ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 110; DB 25
Pred. No. 8.6e-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 173;
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                                                      identification,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CC second nucleic acid molecule comprising any of 15112 nucleotide
CC sequences, appearing as ABX34836-ABX4947, or complements of them.
CC Also included are; (1) a transformed cell having a nucleic acid
CC comprising an IMFD nucleic acid linked to a promoter and a 3' non-
CC translated sequence that functions in the cell to cause termination of
CC transcription and addition of polyadenylated ribonucleotides to a 3' end
CC molecule in a bovine cell or tissue comprising; (a) incubating a marker
CC molecule in a bovine cell or tissue comprising; (a) incubating a marker
CC complement or fragment) with a complementary nucleic acid sequences or its
CC complement or fragment) with a complementary nucleic acid molecule
CC marker nucleic acid and the complementary nucleic acid melecule
CC marker nucleic acid and the complementary nucleic acid melacule;
CC complementary nucleic acid, where the detection of the complementary
CC complementary nucleic acid is used for detecting the level or pattern of the
CC complementary nucleic acid is used for determining a level or pattern
CC of a molecule in a bovine cell or tissue. It is useful for genome
CC mapping, gene identification and analysis, cattle breeding, preparation
CC improving cattle. The present sequence is one of the 15112 bovine
CC LMFD EST (expressed sequence tag) nucleic acid acides
CC LMFD EST (expressed sequence tag) nucleic acide acides
CC LMFD EST (expressed sequence tag) nucleic acide acides
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                    Query Match
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(MATH/)
(TAON/)
                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                         Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?DocID=20020137139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deposition, useful for genome mapping, analysis, cattle breeding, or for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from cattle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a purified nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; SEQ ID No 5962; 245pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-110599/10
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11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-SEP-2001; 2001US-0960352
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                                                                                                                                                                                                                                                                                                    Local Similarity
                       618
                                                                                                                                                                     498
                                                                                                                                                                                                                                                                               211;
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                                                                                                                                  78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) BYATT J C.
) MATHIALAGAN N.
) TAO N.
ATTTAACGGGTCCCCAATTTNATCCNGAACCCANTTTTCCCCCNAACCATANTTACCATT
                                                                                                                                                                                                                                            ANCTATNGAAAANTNGATTANNGACTTGAATTGCCAACCCTANTTNCNGGCCACCNGTGG
                                                                                                                                                                                                                                                                                                                                                        397 BP; 144 A; 75 C; 45 G; 133 T; 0 other;
                                                           TAATCTTCAAATATACATTATTAGCAAAATGAGAGCTTCT--GTTTACATACT-TTTTGT
                                                                                                                                  ATGATATTCTGTTTCTTCATTCTCCCAAGGAAAACT-----TGAAATTTCGGCAGAA
                                                                                                                                                                 GCNTNGTNTTCCTTACTTANTCCCCCCCAAGGAAANNCCTTAANCNGAANCTCCNCCAAAA 557
                                                                                                                                                                                                        TAACCCTTAANTATCCTTGGTAACCAAANCAAAACCTTTTTNGTTTACNTANTCCTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or muscle and
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and the LMFD nucleic acid can specifically hybridise
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                                                                                                                                                                                                                                                                                                  Score 84.6; DB 25; Pred. No. 1.1e-10;
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                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                 167;
                                                                                                                                                                                                                                                                                                                  Length 397;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated with derived
                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                               Gaps
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                       677
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RESULT 10
ABX48095/c
ID ABX480
XX ABX480
XX ABX480
XX Bovine
XX Bovine
XX Bovine
XX Bovine
XX US2002
XX US2002
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XX L2-JAN
PR 11-JAN
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PA (MATH/
PA (MATH/
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PA (M
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The invention relates to a purified nucleic acid molecule associated with CC lactation or muscle and fat deposition (designated LMFD), derived CC from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide CC sequences, appearing as ABX34836-ABX4947, or complements of them. CC Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a3 non-cc translated sequence that functions in the cell to cause termination of CC transcription and addition of polyademylated ribonucleotides to a 3 end CC molecule in a bovine cell or tissue comprising: (a) incubating a marker CC complement or fragment) with a complementary nucleic acid sequences or its complement from the bovine cell or tissue, where hybridisation between the CC marker nucleic acid and the complementary nucleic acid permits the CC complementary nucleic acid of the molecule; and (b) detection of the complementary nucleic acid permits the CC complementary nucleic acid, where the detection of the molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid associated with lactation, and muscle and deposition, useful for genome mapping, gene identification analysis, cattle breeding, or for genetically improving cat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine; ss; EST; expressed sequence tag; muscle deposition; fat deposition; genome gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Byatt JC,
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11-JAN-2000; 2000US-0480902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WARREN W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAO N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID No 13260; 245pp; English
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New nucleic acid associated with lactation, deposition, useful for genome mapping, gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene analysis; cattle breeding.
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11-JAN-2000;
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  and muscle and identification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a purified nucleic acid molecule associated with CC lactation or muscle and fat deposition (designated LMPD), derived CC from cattle, and the LMPD nucleic acid can apecifically hybridise to a second nucleic acid molecule comprising any of 1512 nucleotide CC sequences, appearing as ABX34836-ABX49947, or complements of them. CC Also included are; (1) a transformed cell having a nucleic acid CC comprising an LMPD nucleic acid linked to a promoter and a 3' non-cc comprising an LMPD nucleic acid linked to a promoter and a 3' end CC file mRNA molecule; and (2) determining a level or pattern of a cC nucleic acid (comprising any of the 1512 nucleic acid sequence or its complement or fragment) with a complementary nucleic acid sequence or obtained from the bovine cell or tissue comprising; (a) incubating a marker complement or fragment) with a complementary nucleic acid molecule; and (b) detecting the level or pattern of the complement ary nucleic acid and the complementary nucleic acid permits the cC marker nucleic acid is used for detection of the complementary nucleic acid is predictive of the level or pattern of the complementary nucleic acid is used for determining a level or pattern of the complementary is a marker nucleic acid is used for determining a level or pattern of the complementary nucleic acid is used for determining a level or pattern of the complementary used for determining a level or pattern of the complementary used for determining a level or pattern of the complementary used for determining a level or pattern of the complementary used for determining a level or pattern of the complementary used for determining a level or pattern of the complementary used for determining a level or pattern of the complementary used for determining a level or pattern of the complementary used for determining a level or pattern of the complementary used for determining a level or pattern of the complementary used for determining a level or pattern of the complementary used for determining a le
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                 Brain; placenta; bone marrow; genetic analysis; gene mapping; detection; homology; human; adrenal tissue; ds.
                                                                             Human genome
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23-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATTTTACCTTGGTAAGGCNCAGTNGTTTGCANTNCCGCAAANCAGTANTNTTCC-CCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGGATTTAACGGGTCCCCAATTTNATCCNGAACCCANTTTTCCCCCCNAACCATANTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGAATAGTCTTCAAATATACATTATTAGCAAAATGAGAGCTTCT--GTTTACATACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAAATAACCCTTAANTATCCTTGGTAACCAAANCAAAACCTTTTTNGTTTACNTANTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID No 13016; 245pp; English
                                                                                                                                                                                                                                                                                                                                                                            CCCCCNCCTTTGGCCCAGGNNTTNTTCCCGTCTAAATCCGAACAATAAAA 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cattle breeding, or for genetically improving cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                       (updated)
                                                                             fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 A; 57 C; 80 G; 136 T; 0 other;
                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.3%;
                                                                                                                       entry)
                                                                                                                                                                                                                               263
                                                                                                                                                                                                                                 ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 69.6; DB 25; Pred. No. 4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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RESULT 13
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Best Local S
Matches 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human nucleic acid fragments, isolated from brain adrenal tissue, the placenta or bone marrow comprise any of: (A) a sequence selected from (AAQ76401-Q77613), (B) an allelic variation of a sequence as described in (A), or (C) a sequence complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence as
to (A) or (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 64; 616pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid fragment for genetic analysis and m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gross J,
         WO200160860-A2
                                                 pharmacogenomic
                                                            Human; prostate
                                                                                  Human prostate expression marker cDNA 60907.
                                                                                                        13-SEP-2002
                                                                                                                                                 ABV60916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-035056/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUL-1993;
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                                                                                                                                                                                                                                                                     643
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153; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263
                                                                                                                                                standard; cDNA; 340
                                                                                                                                                                                                      GCAATTGCAAAA 19
                                                                                                                                                                                                                         GCANTNCCGCAA 714
                                                                                                                                                                                                                                               GAAACTCGATTTTACNNCCAA--ACCATAATTACTATTAATTTGTAATGCACAGTTGTAT
                                                                                                                                                                                                                                                                                                           AAANCAAAACCTTTTTNGTTTACNTANTCCTTGGGATTTAACGGGTCCCCAATTTNATCC
                                                                                                                                                                                                                                                                                                                                    ACGAGGAAAACTCTTAAACTGAATCTTAGCAGAAAATCC--
                                                                                                                                                                                                                                                                                                                                                         CCAAGGAAANNCCTTAANCNGAANCTCCNCCAAAATAACCCTTAANTATCCTTGGTAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                  NGAACCCANTTTTCCCCCCNAACCATANTTACCATTTTACCTTGGTAAGGCNCAGTNGTTT
                                                                                                                                                                                                                                                                                          AAAACAAAAGCTTTTTTTTTTTACATCGTTCTTTTGGATTTTTATTGTTTTTTATTTTTATTCT
                                                                                                                                                                                                                                                                                                                                                                              TGGAGTACACAGCACTGATTACTGGCCAGCTGTTGGCATTGTGTTTC-TACTTAGTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                    TTGAATTGCCAACCCTANTTNCNGGCCACCNGTGGGCNTNGTNTTCCTTACTTANTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hadfield KM,
Starkey M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (B)
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                       (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93WO-GB01467
                                                 marker; gene;
                                                            cancer; cytostatic; carcinogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 A; 38 C;
                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 8.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      t encoding mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 69.4; DI
Pred. No. 4e-0
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  4; DB 15;
4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 products -
                                                                                                                                                                                                                                                                                                                                                                                                                         92;
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                                                            pharmacodyanamic
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be used
                                                                                                                                                                                                                                                                                                                                                                                                                                               263;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                             marker;
                                                                                                                                                                                                                                                                                                                                                         582
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RESULT 14
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Best Local S
Matches 127
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16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
21-MAY-2002
                          ABK40018;
                                                     ABK40018 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) a seful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, used for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 11581; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient, assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-662795/76.
                                                                                                                         296
                                                                                                                                                     472
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                                                                                                                                                                                                                                                                                                                     NCCCNNNTTAAAANTNTTTTNATTTAAAAATAACCCNGTNTCCAACCCCNGATCANATT
                                                                                                                                                                                                                                                                                                                                                                         GGTCCAATTATCCTNAANGAGGGNNTTTNANNACTAATNCCCNGATTTTCCAATANGGAA
                                                                                                                                                                                GAAATTTTTAAACCCCGGGGTTTAAAAACCCCCCCCAAATTTTTTTGGGGGGCCTTTTTGC
                                                                                                                                                                                                    AAATTTTTAACCCCCCTANTTTTAAAANCTATNGAAAANTNGATTANNGACTTGAATTGC
                                                                                                                                                                                                                                      CCTTTNATTTGGATTGGGGAAAAAATNCNGTTCCNNATACCNNGAANNGCAAANTTTTT
                                                                                                                                                                                                                                                                                           CCCCCCCTGGGGGGGCCCCCCGGG
                                                                                                                                                     CAACCCTANTINCNGGCCACCNGTG
                                                                                                                                                                                                                                                                                                                                                 ĠĠĠĄĄĄĄĄĄĄĆĊŤTĠĠĠĠĠĠĠĠĠŦŤŤĄĄĄĄĄĊĊĠĊĊĊĊŢŢŢŤŤŤĊĊĊĄĄĄĄĠĠĠĄ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            вP;
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                                                                                                                                                                   8.2%;
                                                    DNA; 18133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 81 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 G;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 69.4;
Pred. No. 4.
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                                                                                                                         320
                                                                                                                                                     496
                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                   4; DB 23;
4.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                340;
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                                                                                                                                                                                                                                                                                           175
                                                                                                                                                                                                                                                                411
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AAATANTTAACCTTNCTTGAAAANGGAAATTTNTACCAANGGACNGAAANCNTTNTAATT 184

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                                                                                                                                                                                                The invention relates to a nucleic acid comprising a sequence at CC least 18 bases in length of a segment of the chemically pretreated DNA CC of genes associated with pharmacogenomics according to one of the Sequences of the genes ALDH6 (NM 000693), CYP11A (NM 000781), CYP11B1 (CC (NM 000497), CYP3A3 (NM 00776 and NM 017460), DPYD (NM 000110), EPHX2 (NM 001979), OCIN (NM 002538), TXNRDI (NM 003330), UCTB (NM 003360), CC (NM 01979), OCIN (NM 019901, NM 019902, NM 019862, NM 019898, CC (NM 01989) and their complementary sequences, or a sequence (SI) chosen CC from 87 sequences and their complements. The chemical pretreatment CC is bisulphite treatment to convert cytosines (but not methyl-cytosines) into uracils. Also included are an oligomer (II) in particular an CC oligomuclectide or a peptide nucleic acid (PNA)-oligomer, comprising in CC each case at least one base sequence having a length of 9 nucleotides CC which hybridises to or is identical to a chemically pretreated DNA of Genes associated with pharmacogenomics and their complements, arranged in CC can array for analysing diseases associated with the methylation state (CC (CpG) and/or detecting SNPs (single nucleotide polymorphisms) cof the 87 sequences. The oligomers may also be used as PCR primers. CC of the 87 sequence data for this patent did not form part of the printed specification, but was obtained in electronic for mat directly from WIPO at CC fro.wiso. int/pub/published but segmences.
                                                                                                                                    Query Match
Best Local (
                                                                                                                    Matches 174;
                                                                                                                                                                                              Sequence 18133 BP; 5519 A; 331 C; 3750 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; treytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TrugT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 100; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human chemically pretreated gene sequence #50
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                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPIGENOMICS AG
NCNCNCNGANTTTNANAAANTACCTTTNNTNTTAAAAAACCTNGGAAAAAAAATAATNGC
                                                                            AAAAAANTTATTTNAATTTCCTATTAANCNTCCTCCNCAAANCATTATTTNACCCTATN
                                        Piepenbrock C,
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000DE-1032529
2000DE-1043826
                                                                                                                                    7.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berlin
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                                                                                                                  Score 61.8; DB 24;
Pred. No. 7.3e-05;
0; Mismatches 260;
                                                                                                                                                                                                8533 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strand
                                                                                                                                                        Length 18133;
                                                                                                                    Indels
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                                                                                                                    Gaps
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    124
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RESULT 15
ABL32941/c
ID ABL329
XX ABL329
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XX O1-JAN
XX O2-JUL
XX O2-JUL
XX O2-JUL
XX O1-SEP
XX 
                                                       The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, named, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, including arthritis, psoriasis, and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antisoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; ana acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy neurofibromatosis; rheumatoid arthritis; psoriasis; bowel di
                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-130909/17.
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01-SEP-2000; 2000DE-1043826
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                                                                  TTGGGGAAAAAATNCNGTTCCNNATACCNNGAANNGCAAANTTTTTAAATTTTTAACCC
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                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                   Published Applications NA:*

1: /cgn2_6/ptcdata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptcdata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptcdata/1/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptcdata/1/pubpna/US07 NEW PUB.seq:*

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10: /cgn2_6/ptcdata/1/pubpna/US09 PUBCOMB.seq:*

10: /cgn2_6/ptcdata/1/pubpna/US09E PUBCOMB.seq:*

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11: /cgn2_6/ptcdata/1/pubpna/US09E PUBCOMB.seq:*

12: /cgn2_6/ptcdata/1/pubpna/US09 NEW PUB.seq:*

13: /cgn2_6/ptcdata/1/pubpna/US10A PUBCOMB.seq:*

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SUMMARIES
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Description	Sequence 22, Appl	Sequence 3296, Ap	Sequence 19, Appl	Sequence 20, Appl	Sequence 7228, Ap	Sequence 7228, Ap	578,	Sequence 161, App		•	Sequence 5962, Ap	Sequence 13260, A	Sequence 13016, A	Sequence 914, App	1922	Sequence 1979, Ap

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Sequence 739, App	100,	e 520,	e 1461,	æ	e 1366	e 71,	Sequence 2053, Ap	e 1118	1329	Sequence 7, Appli	2143		141	Sequence 1, Appli	1143		Sequence 130, App		Sequence 2119, Ap	309,	ce 2, A	e 1393,	Sequence 159, App	e 181, /	e 638	Sequence 2, Appli	Sequence 1122, Ap

ALIGNMENTS

	; OTHER INFORMATION: n = a, c, g or t	; LOCATION: (47)(47)		; OTHER INFORMATION: n = a, c, g or t	; LOCATION: (42)(42)	; NAME/KEY: Unsure	; OTHER INFORMATION: n = a, c, g or t	; LOCATION: (35)(35)	; NAME/KEY: Unsure	; OTHER INFORMATION: n = a, c, g or t	; LOCATION: (33)(33)	; NAME/KEY: Unsure	; OTHER INFORMATION: n = a, c, g or t	; LOCATION: (19)(19)	; NAME/KEY: Unsure	О	; LOCATION: (12)(12)	; NAME/KEY: Unsure	; FEATURE:	; ORGANISM: Homo sapiens	; TYPE: DNA	; LENGTH: 843	; SEQ ID NO 22 ·	; SOFTWARE: PatentIn version 3.0	; NUMBER OF SEQ ID NOS: 87	FILING DATE: 1997-07-17	; PRIOR APPLICATION NUMBER: US 08/896,164	; CURRENT FILING DATE: 2001-04-16	; CURRENT APPLICATION NUMBER: US/09/835,992A	OF INVENTION: METHODS FOR DIAGNOSING AND TREA	ATED NUCLEIC ACID MOLECULES	; APPLICANT: Obata, Yuichi	; GENERAL INFORMATION:	Patent No. US20020037541A1	; Sequence 22, Application US/09835992A	RESULT 1	
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OTHER INFORMATION: n = a
NAME/KEY: Unsure
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APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-5028-W0
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR PILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3296
LENGTH: 1052
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
COTHER INFORMATION: Genbank Accession No. US2002
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APPLICANT: Obata, Y
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Patent No. US20020037541A1
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CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 08/896,164
PRIOR FILING DATE: 1997-07-17
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GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE REFERENCE: 2071.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/190,479
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Pred. No. 1.4e-89;
0; Mismatches 190;
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  RESULT 6
US-10-040-862-7228
; Sequence 7228, Application US/10040862
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PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,79
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,378
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Best Local Similarity
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SEQ ID NO 7228
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Pred. No. 3.6e-67;
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PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 7228
LENGTH: 506
TYPE: DNA
ORGANISM: Homo sapiens
US-10-040-862-7228
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PRIOR FILLING DATE: 2000-03-01
PRIOR PELLORITON NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILLING DATE: 2000-04-27
PRIOR PELLORITON NUMBER: US 60/200,303
PRIOR PELLORITON NUMBER: US 60/200,303
PRIOR PELLORITON NUMBER: US 60/200,303
PRIOR PELLORITON NUMBER: US 60/200,779
PRIOR PELLORITON NUMBER: US 60/200,799
PRIOR PELLORITON NUMBER: US 60/200,999
PRIOR PELLORITON NUMBER: US 60/200,999
PRIOR PELLORITON NUMBER: US 60/200,999
PRIOR PELLORITON NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR PELLORITON NUMBER: US 60/206,201
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR PELLORITON NUMBER: US 60/206,201
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Best Local
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APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/218,950 FILING DATE: 2000-07-14
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                         AAAANTNTTTNATTTTAAAAATAACCCNGTNTCCAACCCCNGATCANATTCCTTTNATT
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APPLICANT: Xu, Jiangchun

APPLICANT: Chenault, Ruth A.

APPLICANT: Chenault, Ruth A.

APPLICANT: Meagher, Madelein Joy

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.561

CURRENT APPLICATION NUMBER: US/09/998,598

CURRENT FILING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 2606

SOFTWARE: COTixa Invention Disclosure Database

SEQ ID NO 578

LENGTH: 486
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; ORGANISM: Homo
US-09-998-598-578
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Best Local Similarity
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TNCNGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAAAAAAANTTATTTNAATTTCCTATTAANCNTCCTCCNCAAANCATTATTTNACCCTA
                                      CTCACTAATTTTAAGAACTATTGAGAAATTGATTAATGACATGAAGTGCACAACACTAAT
                                                                  CCCCCTANTTTTAAAANCTATNGAAAANTNGATTANNGACTTGAATTGC-CAACCCTANT 481
                                                                                                                          GATTTGGGAAGAAATACTGTTTCTGATAGCATGAAATGCAAAATTTTTAGATTTTTAAT
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72.8%;
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Pred. No. 6.3e-66;
D; Mismatches 131;
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SEQ ID

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US-10-102-524-161/c

Sequence 161, Application US/10102524

Publication No. US20030109434A1

GENERAL INFORMATION:

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Gaiger, Alexander

APPLICANT: Gordon, Brian

APPLICANT: Harlocker, Sugan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CAN

FILE REFERENCE: 210121.572

CURRENT APPLICATION NUMBER: US/10/102,524

CURRENT APPLICATION NUMBER: US/10/102,524

CURRENT FILING DATE: 2002-03-19

NUMBER OF SEQ ID NOS: 1863

SOPTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 161

LENGTH: 510

TYPE: DNA

ORGANISM: Homo sapiens
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Gaiger, Alexander
APPLICANT: Gordon, Brian
APPLICANT: Gordon, Brian
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CAN
FILE REFERENCE: 210121.572
CURRENT APPLICATION NUMBER: US/10/102.524
CURRENT APPLICATION NUMBER: US/10/102,524
CURRENT APPLICATION NUMBER: 3002-03-19
NUMBER OF SEQ ID NOS: 1863
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                       US-10-102-524-188/c
US-10-102-524-188/c
; Sequence 188, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
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Best Local Similarity 69.5%;
Matches 248; Conservative
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US-10-102-524-645
; Sequence 645, Application US/10102524
; Publication No. US20030109434A1
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                                                                                                                                                                                                                                                                                      LENGTH: 510
TYPE: DNA
ORGANISM: Homo sapiens
US-10-102-524-645
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CURRENT APPLICATION NUMBER: US/10/102,524
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 1863
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 645
LENGTH: 510
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Best Local Similarity
Matches 248; Conserv
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                                                                                                                                                                                                                                Query Match
Best Local (
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APPLICANT: Mannion, Jane
APPLICANT: Gaiger, Alexander
APPLICANT: Gordon, Brian
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS F
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQ ID NO 188
LENGTH: 510
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                Local Similarity
                                                                                         552 CCAAAATAACCCTTAANTATCCTTGGTAACCAAANCAAAACCTTTTTNGTTTACNTANTC 611
                                                                                                                                                               492 CNGTGGGCNTNGTNTTCCTTACTTANTCCCCCCCAAGGAAANNCCTTAANCNGAANCTCCN 551
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                        CTTGGGATTTAACGGGTCCCCAATTTNATCCNGAACCCANTTTTTCCCCCCNAACCATANTT
                                                                   GCAGAATAATCCTTAAATATACTTTGTAAGCAAAACAAAAGCTTTTTTGTTTACATAGTT 120
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milarity 69.5%;
Conservative
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                                                                                                                                                                                                            Score 182.2; DB 14;
Pred. No. 3.9e-34;
0; Mismatches 104;
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                                                                                                                                                                                                                                                 DB 14;
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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION UNUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5962
LENGTH: 397
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 26-LIB188-014-Q1-E1-G5
US-09-960-352-5962
RESULT 12
US-09-960-352-13260/c
; Sequence 13260, Application
; Patent No. US20020137139A1
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US-09-960-352-5962
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Best Local Similarity
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                                                                                                            GCTATTTCCCAATGTAGAGTTTCAATCTAA
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                                                                                                                                                                                                                       TTTCCCCCGANCCTTGGGAAAAACGGGATNGGTCCCCCCTTAAAAAAACAACCTTCCCCC
                                                                                                                                                                                                                                                                                             TTACCTTGGTAAGGCNCAGTNGTTTGCANTNCCGCAAANCAGTANTNTTCC-CCNGGCNC
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                   US/09960352
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Pred. No. 1.4e-10;
0; Mismatches 167;
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US-09-960-352-13016/c
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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 13260
LENGTH: 449

CENTRAL TARREST CONTRACTOR OF TARREST CONTRACTOR OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                   SEQ ID NO 13016
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Patent No. US20020137139A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 139; Conserv
                                                                             Matches 163;
                                                                                                                                                                                                                                                                                APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TILE OF INVENTION: MUSCLE AND FAT DEPOSITION
TILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER: OF SEQ. ID NOS: 15112
                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Warren, Wesley C. APPLICANT: Tao, Nengbing
                                                                                                                                                                             TYPE: DNA ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 56-BOVMS1-016-Q1-E1-F8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone
                                                                                                                                                                                                                                               LENGTH: 397
                                                                                                  Local Similarity
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                                  CAAAATAACCCCTTAANTATCCTTGGTAACCAAANCAAAACCTTTTTNGTTTACNTANTCC 612
CAGAATAGTCTTCAAATATACATTATTAGCAAAATGAGAGCTTCT
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Pred. No. 5.2e-09;
0; Mismatches 106;
                                                                             Score 69.6; DB 10
Pred. No. 5.8e-07;
); Mismatches 123
                                                                                                                   DB 10;
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                                                                                                                     Length
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TITLE OF INVENTION: Diagnosis of Diseases Ass
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013 1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR PELICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 914
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US-10-311-455-914/c
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Best Local Similarity 40.1
Matches 174; Conservative
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Publication No. US20030143606A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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15939 TCCAAATTATCACACAAAATAACAAAATTAAAAAAACAATACTATTTCTTTATTTTACA
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Pred. No. 0.00036;
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Search completed: November 27, Job time : 320.882 secs
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases As:
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CCURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: PCT/EP01/07537
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 1003529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
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US-10-311-455-1922/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 116; Conserv
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LENGTH: 18218
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                                                                       TTTTTTAAATTCCTTATAAAACTTTTTTTTTTTTAA 3788
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match Length
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/pCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfIles1.seq:*
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   Sequence 22, Appl Sequence 29, Appl Sequence 20, Appl Sequence 14, Appl Sequence 38, Appl Sequence 38, Appl Sequence 1, Appli Sequence 27, Appli Sequence 36, Appli Sequence 37, Appli Sequence 38, Appli Sequence 38, Appli Sequence 31, Appli Sequence 1, Appli 
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                                                                                           APPLICANT: OBATA, Yuichi
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED
TITLE OF INVENTION: WITH GASTRIC CANCER AND METHODS FOR
TITLE OF INVENTION: DIAGNOSING AND TREATING GASTRIC CANCER
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
STATE: New YC
COUNTRY: USA
ZIP: 10022
                                                STREET:
CITY: N
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New York City
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 714 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/89
FILING DATE: July 17, 1997
CLASSIFICATION: 424
ATTORNEY, AGENT INFORMATION:
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MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
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                                 GTTTACATAGTTCTTTGGGATTTTACTGTTCCTAATTTTATTCTGAAACTCAATTTTACC
                                                    GTTTACNTA-NTCCTTGGGATTTAACGGGTCCCCAATTTNATCCNGAACCCANTTTTCCC
                                                                                                ATTGAATCTTCAGCAGAATAATCCTTAAATATACTTTGTAAGCAAAAACAAAAGCTTTTTT
                                                                                                                                                              TTACTGGCCAGCTGTTGGCATTGTGTTTCTTACTTAGTTCTCCCAAGGGAAAACTCTTAA
                                                                                                                                                                                                                                                            CCCCCCTANTTTTAAAANCTATNGAAAANTNGATTANNGACTTGAATTGC-CAACCCTAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATNNCNCNGANTTTNANAAANTACCTTTNNTNTTAAAAAACCTNGGAAAAAAAAATAAT 121
CCNAACCATANTTACCATTTTACCTTGGTAAGGCNCAGTNGTTTGC
                                                                                                                                                                                              TINCNGGCCACCNGTGGGCNTNGTNTTCCTTACTTANTCCCCCCAA-GGAAANNCCTTAA
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IBM PS/2
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73.1%;
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Pred. No. 1.2e-108;
0; Mismatches 187;
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JEL/NDH/SLH
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GCCAAAAAANTTATTTNAATTTCCTATTAANCNTCCTCCNCAAANCATTATTTNACCCT Length 714; Gaps

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; GENERAL INFORMATION:
APPLICANT: OBATA V.
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Best Local Similarity
Matches 495; Conserv
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordberfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/896,164

FILING DATE: July 17, 1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: NO. 6218521man D. Hanson

REGISTRATION NUMBER: JUD 5499 - JE

REFERENCE/DOCKET NUMBER: JUD 5499 - JE

TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES TITLE OF INVENTION: WITH GASTRIC CANCER AND METHODS TITLE OF INVENTION: DIAGNOSING AND TREATING GASTRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                 NNTTTNANNACTAATNCCCNGATTTTCCAATANGGAANCCCNNNTTAAAAANTNTTTTNAT
                                                                                                                             TTATAATTTGAAAACTGCATCTGAAAGCAAACTTTATTGTTCAATTATTCTTAATGATGG
                                                                                                                                               TTATANTTNGAAANCGGCNNCNGAAACCAANCTTNATGGTCCAATTATCCTNAANGAGGG
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Pred. No. 4.4e-102;
0; Mismatches 190;
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US-09-313-294A-1553/c
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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
CURRENT APPLICATION UNSER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 122; Conservat
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Patent No. 6476212
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Inc:
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                                                                                                                                    CACTGAATTTTAAGAAATAACATTAGTATTAGAAAAACTAGGAAAAAAGATAAATGCAGA
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                                                                                                                                                                                                                                                                                               13.0%;
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                                                                                                                                                                                                                                                                              Score 110; DB 4;
Pred. No. 7.3e-21;
0; Mismatches 49
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Sequence 14, Application US/08232463
PATENT NO. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.

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Best Local :
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-08-232-463-14
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FILING DATE: 26-AUG-1991
ATTORNEY, AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 304'
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: RE NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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; Sequence 38, Application US/09302; Patent No. 6333148; GENERAL INPORMATION: APPLICANT: JACOBSON, Myron K. APPLICANT: JACOBSON, Blaine L. APPLICANT: ACOBSON, Blaine L. APPLICANT: AN Jean-Christophe; APPLICANT: LIN, Winston
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SEQ ID NO 38
LENGTH: 29793
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
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PRIOR APPLICATION NUMBER: 2000-02-23
PRIOR APPLICATION NUMBER: 09/302,812
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 38
                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                               APPLICANT: JACOBSON, Myron K. APPLICANT: JACOBSON, Elaine L. APPLICANT: AME, Jean-Christophe APPLICANT: LIN, Winston
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CURRENT APPLICATION NUMBER: US/09/302,812B
CURRENT FILING DATE: 1999-04-30
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                                                                           CURRENT APPLICATION NUMBER: US/09/511,477
CURRENT FILING DATE: 2000-02-23
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                                                                                                                    FILE REFERENCE:
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Pred. No. 0.025;
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CURRENT FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 09/302,812
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 38
LENGTH: 29793
TYPE: DNA
TYPE: DNA
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Patent No. 6395543
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LIN, Winston
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Pred. No. 0.025;
0; Mismatches 206;
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RESULT 9
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TITLE OF INVENTION: Com
Patent No. 6503729
TITLE OF INVENTION: ja:
FILE REFERENCE: PB375
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Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
                                                                                               NAME/KEY: misc feature
LOCATION: (98239). (98239)
OTHER INFORMATION: n equals a
NAME/KEY: misc feature
LOCATION: (98266). (98266)
OTHER INFORMATION: n equals a
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OTHER INFORMATION: n equals a
NAME/KEY misc feature
LOCATION: (84773)...(84773)
OTHER INFORMATION: n equals a
NAME/KEY misc feature
LOCATION: (84808)...(84808)
LOCATION: (98343) . (98343) a OTHER INFORMATION: n equals a NAME/KEY: misc_feature LOCATION: (10398) . (103998) OTHER INFORMATION: n equals a
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CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals
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LOCATION: (84812) ... (84812)
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LOCATION: (98159)..(98159)
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LOCATION: (191995) ... (191995)
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LOCATION: (779455)...(779455)
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals
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*OCATION: (234814)..(234814)
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NAME/KEY: (600992)..(600992)
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LOCATION: (559167)..(559167)
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LOCATION: (309398)..(309398)
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OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (1637998). (1637998)
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LOCATION: (1349473) ...(1349473)
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LOCATION: (1310988)..(1310988)
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LOCATION: (871619)..(871619)
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LOCATION: (1664
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LOCATION: (1602912)..(1602912)
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OTHER INFORMATION: n equals a,
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Ś 밁 Ś 밁 á 문 Ş 밁 8 Query Match 4.9%; Best Local Similarity 42.6%; Matches 121; Conservative 1150365 1150545 1150605 1150485 335 216 156 96 NGAAACCAANCTINATGGTCCAATTATCCTNAANGAGGGNNTTTT-NANNACTAATNCCCN GATTTTCCAATANGGAANCCCNNNTTAAAANTNTTTTNATTTTAAAAATAACCCNGTNTC GGACAACTAATTTCAATGCCTGTATATTCTGTAAGATTCAGTTTAGRAAACTCGAACATT 1150426 TTYACAATCCTAAGTAAAGAACTTCAAAAAATAAACAGTTCAATTACTGTAGATTATAAT TNTACCAANGGACNGAAANCNTTNTAATTNGAANTNAAATTATANTTNGAAANCGGCNNC TTAAAAAGAACTCGCTAAGGCAATAGTTAGAGAAATGGGACAACCAAGGAAAATAGAAACC 1150546 TTAAAAAACCTNGGAAAAAAAATAATNGCAAATANTTAACCTTNCTTGAAAANGGAAATT 155 CAACCCCNGATCANATTCCTTTNATTTGGATTGGGGAAAAAAAT 378 2 Score 41.6; DB 4; Pred. No. 0.79; 2; Mismatches 160; Length 1664976; Indels 1; Gaps 334 274 215 1150366 1150486

RESULT 10 US-09-426-290-1/c

sequence 1, Application US/09426290 Patent No. 6410712

GENERAL INFORMATION:

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                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                       APPLICANT: INSELBURG, J. et al.
TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: JII-002CNCP
CURRENT APPLICATION NUMBER: US/08/213,419B
CURRENT FILING DATE: 1994-03-14
PRIOR APPLICATION NUMBER: US 07/870,506
PRIOR PILING DATE: 1992-04-17
PRIOR FILING DATE: 1992-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 93;
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APPLICANT: Jeffrey Gulcher
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 2345.2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
                       NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 168575
TYPE: DNA
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Local Similarity 42.5%; Pred. No. 0.53;
nee 93; Conservative 0; Mismatches 126; Indels 0;
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PatentIn Ver. 2.0
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RESULT 12
US-07-867-106-2/c
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                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 39.6%;
Matches 113; Conservative
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LOCATION: (3850)..(5835)
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TYPE: DNA
ORGANISM: Plasmodium falciparum
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NAME/KEY: CDS
LOCATION: (2407)..(2439)
NAME/KEY: CDS
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NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                               STATE: F
                                                                                                                                                                                                                                                                                                                                                ZIP: 19103
                      NAME: Feeney, Joanne Longo REGISTRATION NUMBER: 35,13
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Philadelphia
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NUMBER:
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  RICE-0002
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RESULT 13
US-08-446-855A-1/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
                            APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
                                                                                                                                                                                                       ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleotide sequence enco
TITLE OF INVENTION: phosphate synthetase II
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding
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APPLICANT: Flores, Maria V
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REFERENCE/DOCKET NUMBER: 47
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                            ADDRESSEE: Nixon & Vanderhye PC
STREET: 1100 No. 5849573th Glebe Road,
CITY: Arlington
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LOCATION:
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2378..5038
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                   47-80
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                                                                                                                                                                                                                                                                                                              8th Floor
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Best Local Similarity
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US-09-150-741-1/c
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Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09150741 Patent No. 6183996 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stewart et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996
TITLE OF INVENTION: Synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8920 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 08/446,855 EARLIER FILING DATE: 1995-07-06
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: AU93/00617
                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER FILING DATE: 1993-12-02
                                                                                                                                                                                                                                                                                                                                           ENGTH: 8920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity hes 87; Conserv
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ATAAATTAATGATGATGATATAATAAAAACATTTATTAATATTAAACGTAAATATAATTA 8553
                                 AATANTTAACCTTNCTTGAAAANGGAAATTTNTACCAANGGACNGAAANCNTTNTAATTN 185
                                                                     CNCNCNGANTTTNANAAANTACCTTTNNTNTTAAAAAACCTNGGAAAAAAAATAATNGCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAAATTAATGATCATATTTAATAAAAACATTTATTAATATTTAAACGTAAATATAATTA 855:
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ilarity 43.1%;
Conservative
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linear
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                                                                                                                                                                                                                Score 39; DB 3; Le Pred. No. 0.5; 0; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 2; Lo
Pred. No. 0.5;
0; Mismatches 115;
                                                                                                                                                                                                                                                   Length 8920,
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RESULT 15
US-09-426-290-1
US-09-426-290-1
Sequence 1, Application US/09426290
Patent No. 6410712
GENERAL INFORMATION:
APPLICANT: Bergiind Ran Olafsdottir
APPLICANT: Jeffrey Gulcher
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
FILE REFERENCE: 2345-2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 168575
TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                            | NAME/KEY: CDS
| LOCATION: (124058)...(124278)
| NAME/KEY: CDS
| LOCATION: (127009)...(127130)
| NAME/KEY: CDS
| LOCATION: (128910)...(129139)
| LOCATION: (128910)...(129139)
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Search completed: November 27, 2003, 12:32:32
Job time : 65.2227 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: CDS
LOCATION: (21181)...(21403)
NAME/KEY: CDS
LOCATION: (95252)...(95430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                             125878 TCAAATGCTTATATTTATCCTTGCATATGAAATTTGTTTTTTTCTTCCCCACAAA 125937
                                                                              125938 ÁACCATTCCT 125947
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                                                                                                                 219 AACCAANCTT 228
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CDS
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